GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:14:00 ; Search time 7239.48 Seconds
(without alignments)
12559.330 Million cell updates/sec

Title: US-09-830-972-1
Perfect score: 3741
Sequence: 1 attgctcgtctgggcggcgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	772.4	20.6	969	13	BU839934	BU839934 AGENCOURT
	2	767.2	20.5	785	14	CA511870	CA511870 UI-R-FJ0-
	3	753.4	20.1	842	13	BU709149	BU709149 UI-M-EW0-
	4	745	19.9	896	14	CB204418	CB204418 AGENCOURT
C	5	725.6	19.4	796	14	CA504729	CA504729 UI-R-FJ0-
	6	709.8	19.0	805	12	BI730192	BI730192 603349739
	7	709.4	19.0	822	14	CB521332	CB521332 UI-M-GH0-
	8	707.8	18.9	986	13	BU841009	BU841009 AGENCOURT
C	9	684.6	18.3	919	13	BU590898	BU590898 AGENCOURT
	10	673.6	18.0	778	13	BU709106	BU709106 UI-M-EW0-
	11	662.6	17.7	777	14	CA320618	CA320618 UI-M-FW0-
	12	660.4	17.7	802	14	CA320635	CA320635 UI-M-FW0-
	13	659.2	17.6	951	13	BQ892001	BQ892001 AGENCOURT
	14	648.6	17.3	739	13	BU612951	BU612951 UI-M-FR0-
	15	638.4	17.1	742	14	CA320833	CA320833 UI-M-FW0-
	16	638	17.1	638	14	CB576696	CB576696 AMGNNUC:C
	17	633.8	16.9	779	14	CB244702	CB244702 UI-M-FY0-
	18	633.4	16.9	862	9	AU079375	AU079375 AU079375
	19	616	16.5	700	12	BI664179	BI664179 603289106
	20	608.2	16.3	935	13	BQ963057	BQ963057 AGENCOURT
	21	606.8	16.2	751	14	CA315995	CA315995 UI-M-FW0-
	22	605	16.2	673	14	CD349457	CD349457 UI-M-FY0-
	23	604.8	16.2	623	14	CB578453	CB578453 AMGNNUC:C
	24	604.8	16.2	691	13	BU707644	BU707644 UI-M-FR0-
	25	598	16.0	609	14	CB580803	CB580803 AMGNNUC:N
	26	589.2	15.7	914	9	AU079162	AU079162 AU079162
	27	574.2	15.3	782	12	BI739239	BI739239 603359521
	28	570	15.2	810	10	BG668013	BG668013 DRABTB12
	29	568.6	15.2	698	13	BU058441	BU058441 UI-M-FO0-
	30	561	15.0	624	14	CB578355	CB578355 AMGNNUC:N
	31	561	15.0	646	9	AA791734	AA791734 vu08b07.r
	32	561	15.0	964	13	BQ900768	BQ900768 AGENCOURT
	33	560	15.0	3533	11	AK034902	AK034902 Mus muscu
C	34	559.8	15.0	567	12	BI289826	BI289826 UI-R-DK0-
	35	556.8	14.9	717	14	BY756291	BY756291 BY756291
	36	556	14.9	556	14	CB613337	CB613337 AMGNNUC:N
	37	550.8	14.7	588	10	BF563033	BF563033 UI-R-BO1-
	38	547.4	14.6	691	14	CB525239	CB525239 UI-M-FY0-
	39	546.8	14.6	817	14	CA322433	CA322433 UI-M-FX0-
	40	545.8	14.6	630	13	BQ769602	BQ769602 UI-M-FI0-
	41	543.4	14.5	781	14	CA322160	CA322160 UI-M-FX0-
C	42	542	14.5	548	10	BF562389	BF562389 UI-R-BU0-
	43	541.4	14.5	686	10	BB307864	BB307864 BB307864
	44	537.4	14.4	679	12	BI149602	BI149602 602848410
	45	537.4	14.4	708	12	BI157842	BI157842 602923001

ALIGNMENTS

```
RESULT 1
BU839934
LOCUS       BU839934                969 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_8947611 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6329890
            5', mRNA sequence.
ACCESSION   BU839934
VERSION     BU839934.1  GI:24024317
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
            Ph.D.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13783  row: g  column: 11
            High quality sequence stop: 651.
FEATURES             Location/Qualifiers
     source          1. .969
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6329890"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_130"
                     /note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
                     Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
                     Primer: Oligo dT.  Average insert size 1.95  kb.
                     Constructed by ResGen, Invitrogen Corp. Note: this is a
                     NIH_MGC Library."
BASE COUNT      325 a    194 c    192 g    256 t      2 others
ORIGIN

  Query Match             20.6%;  Score 772.4;  DB 13;  Length 969;
  Best Local Similarity   89.6%;  Pred. No. 5.8e-112;
  Matches  878;  Conservative    0;  Mismatches   88;  Indels   14;  Gaps    4;

Qy       2172 CATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTT 2231
              ||||| |||||||||||||| | | ||   ||||||||| ||| ||||||||||||||||
Db          1 CATGAGTGTAGCACTAAAAACATCGGACTCAAAGGAAGAAATTAAAGAGCCTGAAAGTTT 60
```

```
Qy       2232 TAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAA 2291
             |||||||||||| ||||||| |||||||||||||||||||||||| ||||||||||||||
Db         61 TAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAA 120

Qy       2292 AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAA 2351
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        121 AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTATTCAGAAATAGCAAA 180

Qy       2352 ATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGA 2411
             ||| |||||||||||||| || |||  |||||| ||||| |||||||||| ||||||||
Db        181 ATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGTGGATGATTCCTCACCCGAATCTGA 240

Qy       2412 ACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGC 2471
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        241 ACCAGTTGACTTATTTAGTGATGATTCAATTCCTGAAGTCCCACAAACACAAGAGGAGGC 300

Qy       2472 TGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCCAGCACAAA-- 2529
             ||||||||| ||||||||||||||||||||||||||||||||| | || ||||||
Db        301 TGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAACACAACACAAACA 360

Qy       2530 -GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCA 2588
              |||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||
Db        361 TAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAGGAAAGCCATATTTAGAGTCTTTTCA 420

Qy       2589 GCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTGACCAAAAA 2648
             |||||||||||||| |||||||||||||||||||| |||||||||||||||||||||||
Db        421 GCCCAATTTACATATTACAAAAGATGCTGCATCTAATGAAATTCCAACATTGACCAAAAA 480

Qy       2649 GGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTT 2708
             ||||| |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        481 GGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGATGACTT 540

Qy       2709 ACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGAT 2768
             |||||||||||||||||||||| |||||||||||||||||| |||||||||| ||
Db        541 ACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCCGATTCATCTCCCAT 600

Qy       2769 TGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCTAAATTAGC 2828
             |||||||||||||||| |||||||| |||||||||||| ||||||||||||
Db        601 TGAGATAATAGATGAGTTTCCCACATTTGTCAGTGCTANAGATGATTCTCCT-------- 652

Qy       2829 CAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGG 2888
              |||||||||||||| |||||||||||| |||||||||||||||||||| |||| |||||
Db        653 -AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAGCGG 711

Qy       2889 GGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCC 2948
              ||  |||| |||||||||| |||||||||||||||||||||||||||||||| ||||||
Db        712 NGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACATATCC 771

Qy       2949 TAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGC 3008
             |||||||||||| |||||| |||||||||||||| | ||| ||||||||||||||||||||
Db        772 TAAAGATGAAGCACATGTCTCAGATGAATTCT-CAAAAGTAGGTCCAGTGTATCTAAGGT 830

Qy       3009 ATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGT 3068
              || ||| || | | |||| |     |||||| |||| | || ||||||| ||||||
Db        831 GCCCCTATTGCTTCCCAATGGTTTCTGCTTGGAATCTCAAATAG-AATGGGCCACATAGT 889

Qy       3069 TAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGA 3128
```

```
              | || |||||  ||||||| |||||||||| |||||||||||||    | ||||||||
Db        890 TTAACCCAAAGTACTTACGGAAGAAGCAGAGGAAAAACTTCCTTCTTGATCCGAGAAAGA 949

Qy       3129 GGACAGATCCCTGTCAGCTG 3148
              ||   |||||||| ||||||
Db        950 GGGACGATCCCTGACAGCTG 969
```

RESULT 2
CA511870

```
LOCUS       CA511870                785 bp    mRNA    linear   EST 15-NOV-2002
DEFINITION  UI-R-FJ0-cpx-e-15-0-UI.r1 UI-R-FJ0 Rattus norvegicus cDNA clone
            UI-R-FJ0-cpx-e-15-0-UI 5', mRNA sequence.
ACCESSION   CA511870
VERSION     CA511870.1  GI:25002824
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. James Lin, Universtiy of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 REVERSE.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-FJ0-cpx-e-15-0-UI"
                     /tissue_type="embryo"
                     /dev_stage="embryo"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-R-FJ0"
                     /note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
                     UI-R-FJ0 is a cDNA library containing the following
                     tissue(s): rat embryo. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
```

6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

BASE COUNT 251 a 174 c 165 g 193 t 2 others

ORIGIN

Query Match 20.5%; Score 767.2; DB 14; Length 785;
Best Local Similarity 99.2%; Pred. No. 3.9e-111;
Matches 780; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```
Qy       1699 ATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAGGATTCT 1758
             ||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db          1 ATAACAGAGAAGACTATCCCCACAACGTCAAATCCTTTCCTTGTAGCAGTACAGGATTCT 60

Qy       1759 GAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAAC 1818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAAC 120

Qy       1819 ATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAACTGAATGAA 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAACTGAATGAA 180

Qy       1879 GCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCT 1938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCT 240

Qy       1939 ATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCA 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCA 300

Qy       1999 ACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCA 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCA 360

Qy       2059 AGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTT 2118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTT 420

Qy       2119 AGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCACCATATGAAGAAGCCATGAAT 2178
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        421 AGTTATGACAGTATAAAGCTTGAGCCTGAAAATCCCCCACCATATGAAGAAGCCATGAAT 480

Qy       2179 GTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCA 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCA 540

Qy       2239 GCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACA 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACA 600
```

```
Qy       2299 AAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAG 2358
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        601 AAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCANAATTCGAG 660

Qy       2359 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 2418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 720

Qy       2419 GACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATG 2478
              |||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db        721 GACTTATTTAGTGATGATTCGATTCCTGAAGT-CCACANACACAAGAGGAGGCTGTGATG 779

Qy       2479 CTCATG 2484
              ||||||
Db        780 CTCATG 785
```

```
RESULT 3
BU709149
LOCUS       BU709149                842 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  UI-M-EW0-caz-o-10-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone
            IMAGE: 6419553 5', mRNA sequence.
ACCESSION   BU709149
VERSION     BU709149.1  GI:23642332
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 842)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin, Univeristy of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .842
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 6419553"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 15.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_EW0"
```

/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail , is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 275 a 182 c 181 g 202 t 2 others
ORIGIN

Query Match 20.1%; Score 753.4; DB 13; Length 842;
Best Local Similarity 94.2%; Pred. No. 5.8e-109;
Matches 792; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

```
Qy       1677 AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT 1736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT 61

Qy       1737 CCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGT 1796
             |||||||||| |||| |||||||||||||||||| |||||||||  ||||||||||
Db         62 CCTTGTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTTATCAAAGGT 121

Qy       1797 GACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGC 1856
             |||||||||| |||| ||| |||||||||||||| ||||||||||||||||||||||
Db        122 GACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGC 181

Qy       1857 ATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGA 1916
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        182 ATGTGAAAGTGAACTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGA 241

Qy       1917 CTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCC 1976
             |||||||| |||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db        242 CTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCCACAGCACAGCTTTGCCC 301

Qy       1977 ATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGC 2036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGC 361

Qy       2037 ACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCC 2096
              |||||||||||||||||||||| ||||||||||||||| |||||||||| ||||||
Db        362 GCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCC 421

Qy       2097 ACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCC 2156
             ||| |||| |||  |||||||||||||||| |||||||||||||||||||| |||||
Db        422 ACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCC 481

Qy       2157 ACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAA 2216
             |||||||||||||||||| |||||||||||| | | ||   ||||||||| ||| ||
Db        482 ACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACTCAAAGGAAGAAATTAA 541
```

```
Qy       2217 AGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGC 2276
             ||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||
Db        542 AGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGC 601

Qy       2277 GTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTA 2336
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        602 ATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTA 661

Qy       2337 TTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTC 2396
             |||||||||||| |||| |||||||||||||| || |||  |||||| ||||| |||||
Db        662 TTCAGAAATAGCANAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGTGGATGATTC 721

Qy       2397 CTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACA 2456
             |||||| ||||||||||||||||||||||||||||||||| |||||||||| |||||
Db        722 CTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATTCCTGAAGT-CCACA 780

Qy       2457 AACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGT 2516
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        781 NACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGT 840

Qy       2517 A 2517
              |
Db        841 A 841
```

```
RESULT 4
CB204418
LOCUS       CB204418                 896 bp    mRNA    linear   EST 05-FEB-2003
DEFINITION  AGENCOURT_11276017 NIH_MGC_135 Mus musculus cDNA clone
            IMAGE:30138586 5', mRNA sequence.
ACCESSION   CB204418
VERSION     CB204418.1  GI:28241848
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM0041  row: k  column: 11
            High quality sequence stop: 686.
FEATURES             Location/Qualifiers
     source          1. .896
                     /organism="Mus musculus"
                     /mol_type="mRNA"
```

/db_xref="taxon:10090"
/clone="IMAGE:30138586"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_135"
/note="Vector: pCMVSport6.1; Site_1: EcoRV; Site_2: NotI;
Normalized full-length enriched library from pooled mouse
embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5
, and 15.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dT. cDNA
enrichment: >1k bp, Average insert size 1.6k bp.
Normalization (Cot value): 7.5 kb. Priming sequence:
5'GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)3' Tissue contributed by
, David Rowe. Library constructed by ResGen, Invitrogen
Corp."

BASE COUNT 255 a 177 c 193 g 271 t

ORIGIN

Query Match 19.9%; Score 745; DB 14; Length 896;
Best Local Similarity 93.0%; Pred. No. 1.2e-107;
Matches 816; Conservative 0; Mismatches 50; Indels 11; Gaps 3;

```
Qy       2745 AACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGC 2804
             ||||||||| |||||||||| |||||||||||||||| |||||||| ||||||||||
Db         13 AACATTTTCCGATTCATCTCCCATTGAGATAATAGATGAGTTTCCCACATTTGTCAGTGC 72

Qy       2805 TAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAG 2864
             ||||||||||||||||         |||||||||||||| |||||||||||| |||||||
Db         73 TAAAGATGATTCTCCT---------AAGGAGTACACTGACCTAGAAGTATCCAACAAAAG 123

Qy       2865 TGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGA 2924
             |||||||||||||| |||| |||||||| |||| |||||||||| ||||||||||||||||
Db        124 TGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGA 183

Qy       2925 CCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGA 2984
             |||||||||||||||| |||||||||||||||| |||||| |||||||||||||||| |
Db        184 CCTTTCTTTCAAGAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAA 243

Qy       2985 AAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACC 3044
             || |||||||||||||||||||   || ||| || | ||||||| |||||||||||| |
Db        244 AAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATC 303

Qy       3045 TCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAA 3104
             ||| | |||||||||||| |||||||||| ||||| ||||||||||||||||||| ||||
Db        304 TCAAATAGAAATGGGCAACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAA 363

Qy       3105 ACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCT 3164
             |||||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db        364 ACTTCCTTCTGATACAGAGAAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCT 423

Qy       3165 GAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGT 3224
             || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        424 GAATAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGT 483

Qy       3225 GTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAC 3284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAC 543
```

```
Qy       3285 GGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGT 3344
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||
Db        544 GGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGT 603

Qy       3345 GATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGA 3404
              |||||| |||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        604 GATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGA 663

Qy       3405 AGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAA 3464
              |||||| |||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        664 AGTTGCCATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAA 723

Qy       3465 CAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 3524
              |||||||||||||||| ||||||| || ||||||||||||||||||||||||||||||||
Db        724 CAGCACAATAAAAGAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 783

Qy       3525 GTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCC-TTGTTCAATGGTCTGACAC 3583
              | |||||||||||||||||| |||||||| ||||||||| |||||||||||| ||||||
Db        784 G-TTGCAGTGTTGATGTGGGTATTTACTTACGTTGGTGCCTTTGTTCAATGGTTTGACAC 842

Qy       3584 TACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCC 3620
              |||||||||||| ||||||||||||||||||||||||
Db        843 TACTGATTTTAGCCCTGATCTCACTCTTCAGTATTCC 879
```

```
RESULT 5
CA504729/c
LOCUS       CA504729                796 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  UI-R-FJ0-cpx-e-15-0-UI.s1 UI-R-FJ0 Rattus norvegicus cDNA clone
            UI-R-FJ0-cpx-e-15-0-UI 3', mRNA sequence.
ACCESSION   CA504729
VERSION     CA504729.1  GI:24995683
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. James Lin, Universtiy of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
```

Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-35, >POLY_A#Simple_repeat (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .796
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-FJ0-cpx-e-15-0-UI"
/tissue_type="embryo"
/dev_stage="embryo"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-R-FJ0"
/note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; UI-R-FJ0 is a cDNA library containing the following tissue(s): rat embryo. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)
TAG_LIB=UI-R-FJ0
TAG_TISSUE=rat-embryo
TAG_SEQ=CATCTCTACT"

BASE COUNT 179 a 184 c 134 g 297 t 2 others
ORIGIN

Query Match 19.4%; Score 725.6; DB 14; Length 796;
Best Local Similarity 99.3%; Pred. No. 1.4e-104;
Matches 728; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       952 TTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCATCCTCAGAAGGAACAATT 1011
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       733 TCTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCATCCTCAGAAGGAACAATT 674

Qy      1012 GAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTA 1071
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       673 GAAGAAACTNTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTA 614

Qy      1072 AATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAA 1131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       613 AATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAA 554

Qy      1132 GGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTG 1191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       553 GGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTG 494
```

```
Qy       1192 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 1251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 434

Qy       1252 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAA 1311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAA 374

Qy       1312 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 1371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         373 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 314

Qy       1372 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 1431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         313 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 254

Qy       1432 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTT 1491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTT 194

Qy       1492 GGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTG 1551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 GGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTG 134

Qy       1552 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 1611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         133 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 74

Qy       1612 ACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 1671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          73 ACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 14

Qy       1672 AAAATAGAAGAAA 1684
             |||| | || |||
Db          13 AAAAAAAAAAAAA 1
```

```
RESULT 6
BI730192
LOCUS       BI730192                 805 bp    mRNA    linear   EST 20-SEP-2001
DEFINITION  603349739F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5357385 5',
            mRNA sequence.
ACCESSION   BI730192
VERSION     BI730192.1  GI:15707205
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 805)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11908 row: n column: 10
High quality sequence stop: 802.

```
FEATURES             Location/Qualifiers
     source          1. .805
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5357385"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_94"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      266 a    179 c    165 g    195 t
ORIGIN
```

Query Match 19.0%; Score 709.8; DB 12; Length 805;
Best Local Similarity 93.8%; Pred. No. 4.4e-102;
Matches 751; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

```
Qy       1854 AGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT 1913
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 AGCATGTGAAAGTGAACTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT 60

Qy       1914 GGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTTTG 1973
             |||||||||||| |||||||||||||||||||| ||| ||||||||||||||||||||||
Db         61 GGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCCACAGCACAGCTTTG 120

Qy       1974 CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA 2033
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA 180

Qy       2034 AGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATC 2093
             ||| |||||||||||||||||||||| |||||||||||||| |||||||||| |||
Db        181 AGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATC 240

Qy       2094 CCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCC 2153
             |||||| |||| |||  |||||||||||||||| |||||||||||||||||||| ||
Db        241 CCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCC 300

Qy       2154 CCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAAT 2213
             |||||||||||||||||||||| |||||||||||| | | ||   ||||||||| |||
Db        301 CCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACTCAAAGGAAGAAAT 360

Qy       2214 AAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCAT 2273
              |||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Db        361 TAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCAT 420

Qy       2274 TGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAA 2333
```

```
                ||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        421 TGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAA 480

Qy       2334 TTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGA 2393
                |||||||||||||||||||| |||||||||||||| || |||  |||||| ||||| ||
Db        481 TTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGTGGATGA 540

Qy       2394 TTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCC 2453
                ||||||||| ||||||||||||||||||||||||||||||||| |||||||||||||
Db        541 TTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATTCCTGAAGTCCC 600

Qy       2454 ACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGAC 2513
                |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        601 ACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGAC 660

Qy       2514 AGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCC 2570
                |||| | || ||||||    |||||||||||||||| |||||||||||| ||||||||||
Db        661 AGTAACACAACACAAACATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAGGAAAGCC 720

Qy       2571 ATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACAT 2630
                |||||||||||||||||||||||||||||| ||| |||||||||||||||| ||| ||
Db        721 ATATTTAGAGTCTTTTCAGCCCAATTTACATATTACCAAAGATGCTGCATCTACTGAAAT 780

Qy       2631 TCCAACATTGACCAAAAAGGA 2651
                |||||||||||||||||||
Db        781 TCCAACATTGACCAAAAAGGA 801
```

```
RESULT 7
CB521332
LOCUS       CB521332                 822 bp    mRNA    linear   EST 28-MAR-2003
DEFINITION  UI-M-GH0-cem-h-13-0-UI.r1 NIH_BMAP_GH0 Mus musculus cDNA clone
            IMAGE: 6841502 5', mRNA sequence.
ACCESSION   CB521332
VERSION     CB521332.1  GI:29354687
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 822)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .822
```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6841502"
/tissue_type="Whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 233 a 162 c 181 g 246 t
ORIGIN

Query Match 19.0%; Score 709.4; DB 14; Length 822;
Best Local Similarity 92.6%; Pred. No. 5.1e-102;
Matches 771; Conservative 0; Mismatches 51; Indels 11; Gaps 2;

```
Qy       2762 CTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCTA 2821
              |||| |||||||||||||||| |||||||| ||||||||||||||||||||||||||||
Db          1 CTCCCATTGAGATAATAGATGAGTTTCCCACATTTGTCAGTGCTAAAGATGATTCTCCT- 59

Qy       2822 AATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCC 2881
                  |||||||||||||| |||||||||||| |||||||||||||||||||| |||
Db         60 --------AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCC 111

Qy       2882 AAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 2941
              | ||||||||  |||| |||||||||| ||||||||||||||||||||||||||||||
Db        112 AGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 171

Qy       2942 TATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTAT 3001
              |||||||||||||||| |||||| |||||||||||||| ||| ||||||||||||||
Db        172 CATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTAT 231

Qy       3002 CTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCA 3061
              ||||||   || ||| || | ||||||| |||||||||||| |||| | ||||||||||||
Db        232 CTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCA 291

Qy       3062 GCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAG 3121
              ||||||||| |||||  |||||||||||||||||| |||||||||||||||| ||||
Db        292 ACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAACTTCCTTCTGATACAG 351

Qy       3122 AGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTTG 3181
              |||||||||||||||||| |||||||||||||||||||| ||||||||||||
```

```
Db        352 AGAAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCTGAATAAAACTTCAGTTG 411

Qy       3182 TTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTAT 3241
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 TTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTAT 471

Qy       3242 TCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGG 3301
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        472 TCCTGCTGCTGTCTCTGACAGTGTT--TCATTGTCAGTGTAACGGCCTACATTGCCTTGG 529

Qy       3302 CCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGA 3361
              |||||||||| |||||||||||||||||||||||||||||| |||||||| ||||||||||
Db        530 CCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGA 589

Qy       3362 AATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGG 3421
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        590 AATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCAGAGG 649

Qy       3422 AATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAAC 3481
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        650 AATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAAT 709

Qy       3482 TGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGT 3541
              ||||||| || |||||||||||||| ||||||||||||||||||||||||||||||||||
Db        710 TGAGGCGTCTCTTCTTAGTTGATGACTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGT 769

Qy       3542 GGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTA 3594
              |||| |||||||| |||||||||||||||||||| |||||||||||| ||||
Db        770 GGGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGACTTTA 822
```

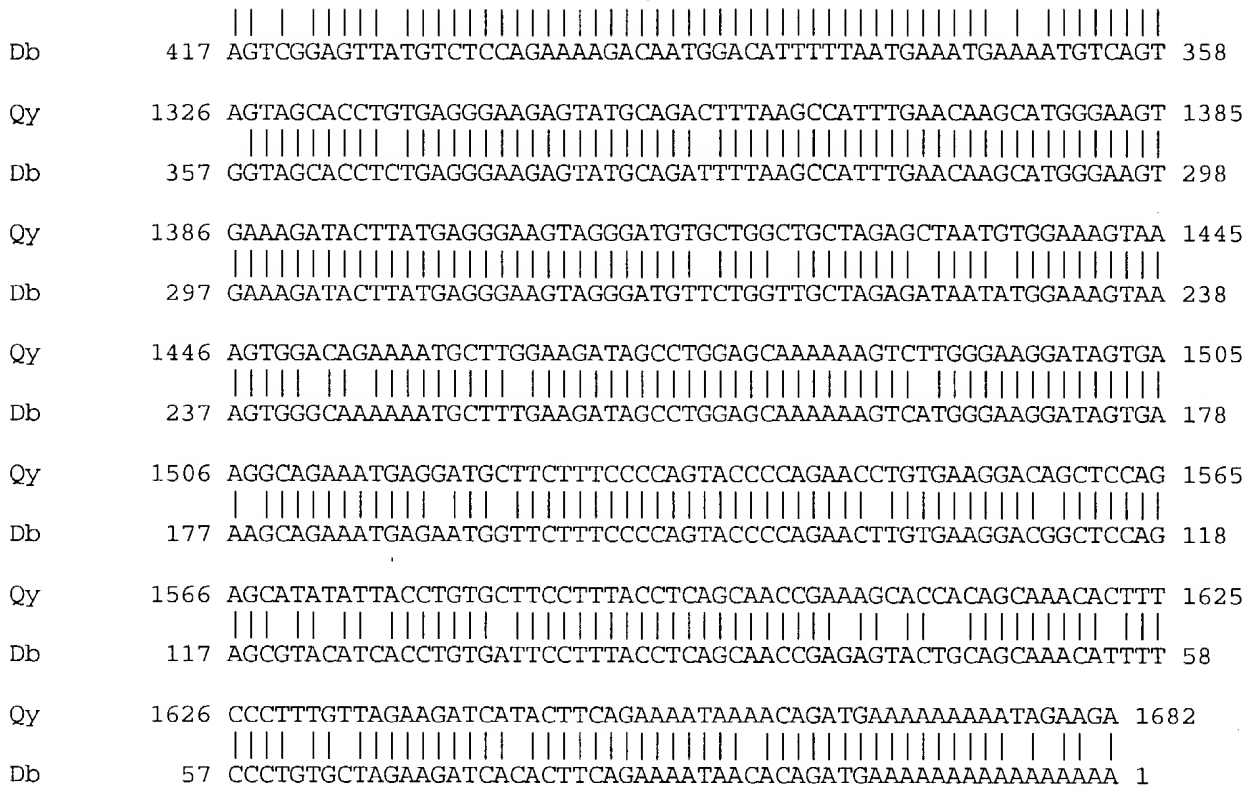
```
RESULT 8
BU841009
LOCUS       BU841009                986 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_10187690 NIH_MGC_134 Mus musculus cDNA clone
            IMAGE:6518816 5', mRNA sequence.
ACCESSION   BU841009
VERSION     BU841009.1  GI:24025409
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14101  row: c  column: 09
```

```
            High quality sequence start: 21
            High quality sequence stop: 644.
FEATURES             Location/Qualifiers
     source          1. .986
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6518816"
                     /tissue_type="undifferentiated limb"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_134"
                     /note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
                     NotI; Cloned unidirectionally. Primer: Oligo dT. Average
                     insert size 1.7 kb. Constructed by ResGen, Invitrogen
                     Corp. Note: this is a NIH_MGC Library."
BASE COUNT      302 a    227 c    208 g    248 t      1 others
ORIGIN

  Query Match             18.9%;  Score 707.8;  DB 13;  Length 986;
  Best Local Similarity   87.8%;  Pred. No. 8.9e-102;
  Matches  832;  Conservative    0;  Mismatches  103;  Indels   13;  Gaps    5;

Qy       1728 AAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTT 1787
              |||||||||||||||||||| |||| |||||||||||||||||||| ||||||||||  ||
Db         29 AAATCCTTTCCTTGTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTT 88

Qy       1788 ATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGT 1847
              |||||||||||||||||||| |||| ||| |||||||||||||| |||||||||||||
Db         89 ATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGT 148

Qy       1848 TCAGGAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAAC 1907
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        149 TCAGGAAGCATGTGAAAGTGAACTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAAC 208

Qy       1908 AAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACA 1967
              |||||||||||||||||| |||||||||||||||||| ||| ||||||||||||||||
Db        209 AAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCCACAGCACA 268

Qy       1968 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGT 2027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGT 328

Qy       2028 TATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAG 2087
              ||||||||| |||||||||||||||||||||||| |||||||||||||| |||||||||
Db        329 TATGGAAGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAG 388

Qy       2088 TGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGA 2147
              || |||||||||  ||||  |||  ||||||||||||||||  ||||||||||||||||||
Db        389 TGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGA 448

Qy       2148 AAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGA 2207
              |||  |||||||||||||||||||||||||  ||||||||||||  | | ||   |||||||
Db        449 AAATCCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACGCAAAGGA 508

Qy       2208 AGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATAT 2267
              || |||  ||||||||||| |||||||||||||||| |||||||  ||||||||||||||||
Db        509 AGAAATTAAAGAGCCTGANAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATAT 568
```

```
Qy       2268 ATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTT 2327
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        569 ATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTT 628

Qy       2328 CTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGT 2387
             |||||||||||||||||||||||||| |||||||||||||| || |||  |||||| ||
Db        629 CTCTAATTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGT 688

Qy       2388 GGAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGA 2447
             ||| |||||||||| ||||||||||||||||||||||||||||||||| || |||||
Db        689 GGATGATTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATCCCTGA 748

Qy       2448 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC 2507
             |||||||| |||||||||||| |||||||||| ||||| ||||||||||   | ||||
Db        749 AGTCCCACCAACACAAGAGGAAGCTGTGATGCTTATGAAAGAGAGTCTCACCTGAATGTC 808

Qy       2508 TGAGACAGTAGCCCAGC----ACAAAGAGGAGAGACTTAGTG----CCTCACCTCAGGAG 2559
             |||||||||  |||  |    ||| |  |||||||||||||    || | ||  |||
Db        809 TGAGACAGTTACCCCACCCCAACATAAGGGAGAGACTTAGTGCTTTCCCCTCCGGAGGGT 868

Qy       2560 CTAGGAAAGCCATATTTAGAGTCTTTT--CAGCCCAATTTACATAGT--ACAAAAGATGC 2615
               |  |   ||   |||||||||||||     |||||||||| || |   |||| |||||
Db        869 AGAAAAGGCCCTATTTTAGAGTCTTTTTCAGCCCCAATTTACCTATTTACCAAAGGATGC 928

Qy       2616 TGCAT-CTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTT 2662
             ||| | ||||||| | | | || ||   |  ||| | || |   | ||
Db        929 TGCCTCCTAATGAAAATTCCACCTTTGGCCCAAAAGGGAGACCATTTT 976
```

```
RESULT 9
BU590898/c
LOCUS       BU590898                 919 bp    mRNA    linear   EST 20-SEP-2002
DEFINITION  AGENCOURT_8798355 NIH_MGC_137 Mus musculus cDNA clone IMAGE:6430691
            5', mRNA sequence.
ACCESSION   BU590898
VERSION     BU590898.1  GI:23242434
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
             cDNA Library Preparation: Catherine Lee, Endocrine Pancreas
            Consortium
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBD8  row: e  column: 12
```

```
            High quality sequence start: 23
            High quality sequence stop: 123.
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6430691"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_137"
                     /note="Organ: pancreas; Vector: pSPORT1; Site_1: SalI;
                     Site_2: NotI; Library consists of a pool of clones
                     rearrayed from the following libraries: Melton normalized
                     mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
                     islets 1 MIS1-A, and Kaestner ngn3 wt. Clones rearrayed in
                     the laboratory of K. Kaestner (University of Pennsylvania
                     ). Note: this is a NIH_MGC Library."
BASE COUNT      235 a    208 c    162 g    314 t
ORIGIN

  Query Match             18.3%;  Score 684.6;  DB 13;  Length 919;
  Best Local Similarity   88.5%;  Pred. No. 4.1e-98;
  Matches  794;  Conservative    0;  Mismatches   84;  Indels   19;  Gaps    4;

Qy        805 CCTGTGATACCCTCCTCTG--CAGAAAAAATTATGGATTTGATGGAGCA-GCCAGGTAAC 861
              ||||||||||||||||  ||     |||| ||||||||||||| ||||||  |||||||||
Db        897 CCTGTGATACCCTCCCTTGACAGAAAAATATTATGGATTTGAAGGAGCACCCCAGGTAAC 838

Qy        862 ACTGTTTCGTCTGGTC-AAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCT 920
                |||||||||  ||| ||||||||||||||||||||| ||  |||||||| |||||||||
Db        837 CATGTTTCGTCATGTCTAAGAGGATTTCCCATCTGTCGTGTATGAAACTGTTGCCTCTCT 778

Qy        921 TCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTT 980
              ||||  | ||| | || || |||||||||||||||||||||| |||| | ||||||||||
Db        777 TCCTGGTATATATACTATCCCAACTGTTTCTTTTAAAGAACACGGATTCTTTGGTAACTT 718

Qy        981 ATCAGCAGTGTCATCCTCAGAAGGAACAATTGAAGAAACTTTAAATGAAGCTTCTAAAGA 1040
              |||||||||| |||||||||||||||| ||||||| |||||||||||||||||||| |||
Db        717 ATCAGCAGTGGCATCCTCAGAAGGAACTATTGAAGTAACTTTAAATGAAGCTTCTAGAGA 658

Qy       1041 GTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATT 1100
               || ||||||||||||||||||||||||||||||||||| | |||||| ||||||| |||
Db        657 ATTCCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAGTCAGCAGAGTTTTCAGTATT 598

Qy       1101 AGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATT 1160
              |||||| |||||||||||||||||| || || |||||||||||||||||||||| ||
Db        597 AGAATAGTCAGAAATGGGATCATCTTTCAATGGGTCCCCAAAAGGAGAGTCAGCCATGTT 538

Qy       1161 AGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGATTTAGTTTG 1220
              |||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||
Db        537 AGTAGAAAACATTAAGGAAGAAGTAATTGTGAGGAGTAAAGGCAAAGAGGATTTAGTTTG 478

Qy       1221 TAGTGCAGCCCTTCACAGTCCACAAGAATCACCT---------------GTGGGTAAAGA 1265
              |||||||||||||| | ||||||||| ||||||                |||| ||||||
Db        477 TAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGTCCCTTACTAAAGTGGTTAAAGA 418

Qy       1266 AGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGT 1325
```



```
Db        417 AGTCGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGAAAATGTCAGT 358

Qy       1326 AGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGT 1385

Db        357 GGTAGCACCTCTGAGGGAAGAGTATGCAGATTTTAAGCCATTTGAACAAGCATGGGAAGT 298

Qy       1386 GAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAAAGTAA 1445

Db        297 GAAAGATACTTATGAGGGAAGTAGGGATGTTCTGGTTGCTAGAGATAATATGGAAAGTAA 238

Qy       1446 AGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGATAGTGA 1505

Db        237 AGTGGGCAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAAGTCATGGGAAGGATAGTGA 178

Qy       1506 AGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGCTCCAG 1565

Db        177 AAGCAGAAATGAGAATGGTTCTTTCCCCAGTACCCCAGAACTTGTGAAGGACGGCTCCAG 118

Qy       1566 AGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAACACTTT 1625

Db        117 AGCGTACATCACCTGTGATTCCTTTACCTCAGCAACCGAGAGTACTGCAGCAAACATTTT 58

Qy       1626 CCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAAGA 1682

Db         57 CCCTGTGCTAGAAGATCACACTTCAGAAAATAACACAGATGAAAAAAAAAAAAAAA 1
```

RESULT 10
BU709106

```
LOCUS       BU709106                 778 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  UI-M-EW0-caz-g-18-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone
            IMAGE: 6419369 5', mRNA sequence.
ACCESSION   BU709106
VERSION     BU709106.1  GI:23642247
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin, Univeristy of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
```

```
     source          1. .778
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 6419369"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 15.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_EW0"
                     /note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured mRNa was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was size selected according to mRNA size fraction,
                     ligated with EcoR I adaptor, digested with Not I, and then
                     cloned directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     , is GTGCGTGGAA. This library was created for the
                     University of Iowa Mouse Brain Molecular Anatomy Project
                     (BMAP): 'Gene Discovery in the Developing Mouse Nervous
                     System', supported by National Instututes of Mental Health
                     (NIMH), Hemin Chin, Ph.D., program coordinator."
BASE COUNT      250 a    169 c    167 g    190 t      2 others
ORIGIN

  Query Match             18.0%;  Score 673.6;  DB 13;  Length 778;
  Best Local Similarity   93.9%;  Pred. No. 2.3e-96;
  Matches  711;  Conservative    0;  Mismatches   45;  Indels    1;  Gaps    1;

Qy       1753 GATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTG 1812
              |||||||||||||||||||| ||||||||||  |||||||||||||||||||||| ||||
Db             2 GATTCTGAGGCAGATTATGTCACAACAGATAATTTATCAAAGGTGACTGAGGCAGTAGTG 61

Qy       1813 TCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAACTG 1872
              ||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db            62 GCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAACTG 121

Qy       1873 AATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCA 1932
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          122 AACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAGACATCA 181

Qy       1933 GAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCT 1992
              |||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Db          182 GAAGCTATACAAGAGTCAATTTACCCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCT 241

Qy       1993 GAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTC 2052
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          242 GAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCGCCATTAAATTCTCTC 301

Qy       2053 CTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCT 2112
              ||||||||| |||||||||||||||| |||||||||| ||||||||| |||| |||  ||
Db          302 CTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCCACTAGAAGTACCGTCT 361

Qy       2113 CCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCACCATATGAAGAAGCC 2172
```

```
                ||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||
Db        362 CCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCCACCATATGAAGAAGCC 421

Qy       2173 ATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTT 2232
                ||||  |||||||||||||  | | ||   ||||||||| ||| ||||||||||||||||||
Db        422 ATGAGTGTAGCACTAAAAACATCGGACTCAAAGGAAGAAATTAAAGAGCCTGAAAGTTTT 481

Qy       2233 AATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAA 2292
                ||||||||||  |||||||  |||||||||||||||||||||||||  ||||||||||||||||
Db        482 AATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAAA 541

Qy       2293 GAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAA 2352
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        542 GAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTATTCAGAAATAGCAAAA 601

Qy       2353 TTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAA 2412
                ||  |||||||||||||| ||  |||  ||||||  |||||  ||||||||||| |||||||||
Db        602 TTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGTGGATGATTCCTCACCCGAATCTGAA 661

Qy       2413 CCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCT 2472
                |||||||||||||||||||||||||||  ||||||||||| |||||  ||||||||||||||||
Db        662 CCAGTTGACTTATTTAGTGATGATTCAATTCCTGAAGT-CCACANACACAAGAGGAGGCT 720

Qy       2473 GTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTG 2509
                ||||||||  ||||||||||||||||||||||||||||
Db        721 GTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTG 757
```

```
RESULT 11
CA320618
LOCUS       CA320618                 777 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  UI-M-FW0-ccb-k-24-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
            IMAGE: 6817393 5', mRNA sequence.
ACCESSION   CA320618
VERSION     CA320618.1  GI:24538742
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
```

```
     source          1. .777
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 6817393"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FW0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGCGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
BASE COUNT      267 a    153 c    151 g    205 t      1 others
ORIGIN

  Query Match             17.7%;  Score 662.6;  DB 14;  Length 777;
  Best Local Similarity   92.1%;  Pred. No. 1.2e-94;
  Matches  724;  Conservative    0;  Mismatches   50;  Indels   12;  Gaps    2;

Qy       2147 AAAACCCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGG 2206
              |||| |||||||||||||||||||||||| |||||||||||| | | ||   ||||||
Db             1 AAAATCCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACTCAAAGG 60

Qy       2207 AAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATA 2266
              ||| ||| |||||||||||||||||||||||||| ||||||| ||||||||||||||||
Db            61 AAGAAATTAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATA 120

Qy       2267 TATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATT 2326
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||| |
Db           121 TATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGT 180

Qy       2327 TCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAG 2386
              |||||||||||||||||||||||||| |||||||||||||| || |||  |||||| |
Db           181 TCTCTAATTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCG 240

Qy       2387 TGGAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTG 2446
              |||| |||||||||||| |||||||||||||||||||||||||||||||||| |||||||
Db           241 TGGATGATTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATTCCTG 300

Qy       2447 AAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGT 2506
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db           301 AAGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGT 360

Qy       2507 CTGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAG 2563
```

```
                ||||||||||| | || ||||||    |||||||||||||||| |||||||||||| |||
Db        361 CTGAGACAGTAACACAACACAAACATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAG 420

Qy       2564 GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTA 2623
                ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        421 GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTA 480

Qy       2624 ATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATA 2683
                ||||  |||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        481 ATGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATA 540

Qy       2684 CTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTG 2743
                |||||||||||||  |||||||||||||||||||||||||||||||||  ||||||||||
Db        541 CTGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTG 600

Qy       2744 AAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTG 2803
                ||||||||||  ||||||||||  ||||||||||||||||  ||||||||  ||||||||||
Db        601 AAACATTTTCCGATTCATCTCTCATTGAGATAATAGATGAGTTTCCCACATTTGTCAGTG 660

Qy       2804 CTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAA 2863
                ||||||||||||||||          ||||||||||||| ||||||||||| ||||||
Db        661 CTAAAGATGATTCTCCT---------AAGGAGTACACTGACCTAGAAGTATCCAACAAAA 711

Qy       2864 GTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTG 2923
                |||||||||||||  ||||  |||||  |   ||||  |||||||||  ||||||||||||||
Db        712 GTGAAATTGCTAATGTCCAGAGCGGNGGCAATTCGTTGCCTTGCTCAGAATTGCCCTGTG 771

Qy       2924 ACCTTT 2929
                ||||||
Db        772 ACCTTT 777
```

```
RESULT 12
CA320635
LOCUS       CA320635                 802 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  UI-M-FW0-ccb-o-24-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
            IMAGE: 6817489 5', mRNA sequence.
ACCESSION   CA320635
VERSION     CA320635.1  GI:24538759
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 802)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
```

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.

FEATURES Location/Qualifiers

source 1. .802
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6817489"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 275 a 157 c 154 g 213 t 3 others
ORIGIN

Query Match 17.7%; Score 660.4; DB 14; Length 802;
Best Local Similarity 91.6%; Pred. No. 2.7e-94;
Matches 745; Conservative 0; Mismatches 54; Indels 14; Gaps 4;

```
Qy       2148 AAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGA 2207
              |||  |||||||||||||||||||||||| |||||||||||| | | ||   |||||||
Db          1 AAAATCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACTCAAAGGA 60

Qy       2208 AGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATAT 2267
              || ||| |||||||||||||||||||||||||| ||||||| ||||||||||||||||
Db         61 AGAAATTAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATAT 120

Qy       2268 ATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTT 2327
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        121 ATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTT 180

Qy       2328 CTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGT 2387
              |||||||||||||||||||||||||| |||||||||||||| || |||  |||||| ||
Db        181 CTCTAATTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGT 240

Qy       2388 GGAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGA 2447
              ||| ||||||||||| ||||||||||||||||||||||||||||||||| ||||||||
Db        241 GGATGATTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATTCCTGA 300

Qy       2448 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC 2507
```

```
                ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db         301 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTC 360

Qy        2508 TGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGG 2564
                |||||||||| | || ||||||    |||||||||||||||| |||||||||||| ||||
Db         361 TGAGACAGTAACACAACACAAACATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAGG 420

Qy        2565 AAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAA 2624
                |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         421 AAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTAA 480

Qy        2625 TGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATAC 2684
                ||| |||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db         481 TGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATAC 540

Qy        2685 TGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGA 2744
                |||||||||||| ||||||||||||||||||||||||||||||||| ||||||||||
Db         541 TGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGA 600

Qy        2745 AACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGC 2804
                ||||||||| |||||||||  |||||||||||||||| |||| ||| ||||||||||
Db         601 AACATTTTCCGATTCATCTCNCATTGAGATAATAGATGAGTTTCNCACATTTGTCAGTGC 660

Qy        2805 TAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAG 2864
                |||||||||||||||         |||||||||||||| |||||||||||| ||| |||
Db         661 TAAAGATGATTCTCCT---------AAGGAGTACACTGACCTAGAAGTATCCAACACAAG 711

Qy        2865 TGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGA 2924
                |||||||||||||| |||| |||||||||  |||| |||||||||| ||| ||| |||||||
Db         712 TGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGATTTG-CCTGTGA 770

Qy        2925 CCTTTCTTTCAAGAATATATATCCTAAAGATGA 2957
                |||||||||||| | ||| ||||||||||||||
Db         771 CCTTTCTTTCANG-ATACATATCCTAAAGATGA 802
```

```
RESULT 13
BQ892001
LOCUS       BQ892001                951 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8758347 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6315079
            5', mRNA sequence.
ACCESSION   BQ892001
VERSION     BQ892001.1  GI:22284015
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Susan L. Sullivan, PhD.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13744 row: n column: 08
High quality sequence start: 6
High quality sequence stop: 629.

```
FEATURES             Location/Qualifiers
     source          1. .951
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6315079"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_129"
                     /note="Organ: olfactory epithelium; Vector:
                     pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
                     unidirectionally. Primer: Oligo dT. Average insert size
                     2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
                     is a NIH_MGC Library."
BASE COUNT      279 a    186 c    222 g    263 t      1 others
ORIGIN
```

Query Match 17.6%; Score 659.2; DB 13; Length 951;
Best Local Similarity 89.3%; Pred. No. 4.1e-94;
Matches 780; Conservative 0; Mismatches 79; Indels 14; Gaps 6;

```
Qy       2646 AAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGA 2705
              ||| |   ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db         11 AAAAGGAGAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGATGA 70

Qy       2706 CTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCC 2765
              |||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db         71 CTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCCGATTCATCTCC 130

Qy       2766 GATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCTAAATT 2825
              |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db        131 CATTGAGATAATAGATGAGTTTCCCACATTTGTCAGTGCTAAAGATGATTCTCCT----- 185

Qy       2826 AGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAG 2885
                ||||||||||||| |||||||||| |||||||||||||||||||| |||| ||
Db        186 ----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAG 241

Qy       2886 CGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATA 2945
              ||||||  |||| |||||||||| ||||||||||||||||||||||||||||||| |||
Db        242 CGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACATA 301

Qy       2946 TCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAA 3005
              |||||||||||||| |||||| |||||||||||||| ||| ||||||||||||||||||
Db        302 TCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTATCTAA 361

Qy       3006 GGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCAT 3065
              ||   || ||| || | ||||||| |||||||||| |||| | |||||||||| |||
Db        362 GGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAACAT 421

Qy       3066 AGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAA 3125
              ||||||| |||||  |||||||||||||||||| |||||||||||||| ||||||||
```

```
Db        422 AGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAACTTCCTTCTGATACAGAGAA 481

Qy       3126 AGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGA 3185
              ||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||
Db        482 AGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCTGAATAAAACTTCAGTTGTTGA 541

Qy       3186 CCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCT 3245
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 CCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCT 601

Qy       3246 GCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTG-CCTTGGCCC 3304
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        602 GCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCCTTGGCCC 661

Qy       3305 TGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAAT 3364
              ||||||| ||||||||     |||||||||||||||| |||||||| ||||||||||||
Db        662 TGCTCTCTGTGACTATNCAGCTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGAAAT 721

Qy       3365 CAGATGAAGGCCA-CCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAA 3423
              |||||||||||||| ||| |||||||||||||| | |||||||||||| |||||||| |||
Db        722 CAGATGAAGGCCACCCCTTTCAGGGCATATTTGGGATCTGAAGTTGCCATATCAGAAGAA 781

Qy       3424 TTGG-TTCAGAAATACA-GTAATTCTGCTCTTGGTCATGTGAACAG-CACAATAAAAGAA 3480
              |||| |||||||||| | | |||||||||||||| |||| | || | ||||||||||||
Db        782 TTGGTTTCAGAAATATAGGAAATTCTGCTCTTGGGCATGGGGACCGCCACAATAAAAGAA 841

Qy       3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513
              ||  | || | | ||     | | ||  | ||
Db        842 ATGGAGGGGGTCTCCTCCTAAGTTAATGGATTT 874
```

```
RESULT 14
BU612951
LOCUS       BU612951                739 bp    mRNA    linear   EST 20-FEB-2003
DEFINITION  UI-M-FR0-cbd-a-04-0-UI.r1 NIH_BMAP_FR0 Mus musculus cDNA clone
            UI-M-FR0-cbd-a-04-0-UI 5', mRNA sequence.
ACCESSION   BU612951
VERSION     BU612951.1  GI:23279166
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 739)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
```

```
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .739
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="UI-M-FR0-cbd-a-04-0-UI"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FR0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGCGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
BASE COUNT      224 a    148 c    162 g    205 t
ORIGIN

  Query Match             17.3%;  Score 648.6;  DB 13;  Length 739;
  Best Local Similarity   92.9%;  Pred. No. 2e-92;
  Matches  694;  Conservative    0;  Mismatches   44;  Indels    9;  Gaps    1;

Qy       2721 GGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGA 2780
              |||||||||||| |||||||||||||||||||| |||||||||| ||||||||||||||
Db          2 GGAAGACAAAATGAAAGAAAGTGAAACATTTTCCGATTCATCTCCCATTGAGATAATAGA 61

Qy       2781 TGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACAC 2840
              ||| |||||||| ||||||||||||||||||||||||          ||||||||||
Db         62 TGAGTTTCCCACATTTGTCAGTGCTAAAGATGATTCTCCT---------AAGGAGTACAC 112

Qy       2841 TGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATT 2900
              ||| |||||||||||| |||||||||||||||||||| |||| ||||||||  |||| ||
Db        113 TGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTT 172

Qy       2901 GCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGT 2960
              |||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        173 GCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACATATCCTAAAGATGAAGC 232

Qy       2961 ACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCC 3020
              |||||| |||||||||||||| ||| |||||||||||||||||||   || ||| ||
Db        233 ACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTGCT 292

Qy       3021 TTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATC 3080
              | ||||||| |||||||||||| |||| | |||||||||| |||||||||| |||||
Db        293 TCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAACATAGTTAAACCCAAAGT 352
```

```
Qy       3081 ACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCT 3140
             ||||||||||||||||||| |||||||||||||||| ||||||||||||||||||||||||
Db        353 ACTTACGAAAGAAGCAGAGGAAAAACTTCCTTCTGATACAGAGAAAGAGGACAGATCCCT 412

Qy       3141 GTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAG 3200
             | |||||||||||||||||||||||| |||||||||||||||||||||||| ||||||||
Db        413 GACAGCTGTATTGTCAGCAGAGCTGAATAAAACTTCAGTTGTTGACCTCCTGTACTGGAG 472

Qy       3201 AGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGAC 3260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 AGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGAC 532

Qy       3261 AGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTAT 3320
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        533 AGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTAT 592

Qy       3321 CAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCC 3380
             |||||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db        593 CAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCC 652

Qy       3381 ATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAG 3440
             ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||| ||
Db        653 ATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCAGAGGAATTGGTTCAGAAATATAG 712

Qy       3441 TAATTCTGCTCTTGGTCATGTGAACAG 3467
             ||||||||||||||||||||||||||||
Db        713 TAATTCTGCTCTTGGTCATGTGAACAG 739
```

```
RESULT 15
CA320833
LOCUS       CA320833                742 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  UI-M-FW0-ccb-n-23-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
            IMAGE: 6817464 5', mRNA sequence.
ACCESSION   CA320833
VERSION     CA320833.1  GI:24538931
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
```

```
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .742
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 6817464"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FW0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGCGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
BASE COUNT      227 a    149 c    154 g    212 t
ORIGIN

  Query Match             17.1%;  Score 638.4;  DB 14;  Length 742;
  Best Local Similarity   92.6%;  Pred. No. 8.1e-91;
  Matches  696;  Conservative    0;  Mismatches   46;  Indels   10;  Gaps    2;

Qy       2644 AAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGAT 2703
              ||   ||||| |||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          1 AATCTGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGAT 60

Qy       2704 GACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCT 2763
              |||||||||||||||||||||||||| |||||||||||||||||| |||||||||
Db         61 GACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCCGATTCATCT 120

Qy       2764 CCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCTAAA 2823
              || |||||||||||||||| |||||||| ||||||||||||||||||||||||||
Db        121 CCCATTGAGATAATAGATGAGTTTCCCACATTTGTCAGTGCTAAAGATGATTCTCCT--- 177

Qy       2824 TTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAA 2883
                    ||||||||||||| |||||||||| |||||||||||||||||||| ||||
Db        178 ------AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAG 231

Qy       2884 AGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATA 2943
              ||||||||  |||| |||||||||| |||||||||||||||||||||||||||||||| |
Db        232 AGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACA 291

Qy       2944 TATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCT 3003
              |||||||||||||||| |||||| |||||||||||||| ||| ||||||||||||||||
Db        292 TATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTATCT 351
```

```
Qy       3004 AAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGC 3063
             ||||   || ||| || | ||||||| |||||||||||| |||| | |||||||||||| |
Db        352 AAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAAC 411

Qy       3064 ATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAG 3123
             ||||||||| |||||  |||||||||||||||||||| |||||||||||||||| ||||||
Db        412 ATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAACTTCCTTCTGATACAGAG 471

Qy       3124 AAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTT 3183
             |||||||||||||||||| |||||||||||||||||||||| ||||||||||||||||
Db        472 AAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCTGAATAAAACTTCAGTTGTT 531

Qy       3184 GACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTC 3243
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 GACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTC 591

Qy       3244 CTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCC 3303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 CTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCC 651

Qy       3304 CTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAA 3363
             |||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||||
Db        652 CTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGAAA 711

Qy       3364 TCAGATGAAGGCCACCCATTCAGGGCATATTT 3395
             ||||||||||||| ||||||||||||||||
Db        712 TCAGATGAAGGCCA-CCATTCAGGGCATATTT 742
```

Search completed: January 23, 2004, 14:46:28
Job time : 7246.48 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 00:42:43 ; Search time 896.477 Seconds
(without alignments)
11264.762 Million cell updates/sec

Title: US-09-830-972-1
Perfect score: 3741
Sequence: 1 attgctcgtctgggcggcgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3739.4	100.0	4684	21	AAD01173	Rat neurite growth
	2	3739.4	100.0	4684	24	ABN86600	Rat neurotransmitt
	3	2343.6	62.6	4053	22	AAS09453	Human cDNA encodin
	4	2343.6	62.6	4632	24	ABV94680	Human pancreatic c
	5	2333.2	62.4	4093	21	AAA23454	cDNA encoding huma
	6	2323.8	62.1	4822	24	ABS70449	Human bone remodel
	7	2297.4	61.4	4698	25	ABX34563	Human mddt cDNA SE
	8	2289.2	61.2	3579	21	AAZ56886	Human MAGI polypep
	9	2289.2	61.2	3579	22	AAF90324	Human NOGO-A cDNA.
	10	2289.2	61.2	3579	24	ABN86601	Human neurotransmi
	11	2289.2	61.2	3579	24	ABK90134	DNA encoding human
	12	1869.8	50.0	3833	21	AAD01174	Bovine neurite gro
	13	1411.2	37.7	2386	19	AAV30920	Human secreted pro
	14	1408	37.6	2386	22	AAF98399	Human cDNA clone B
	15	1088.8	29.1	1980	22	AAI98079	Human neuroblastom
	16	564	15.1	1568	21	AAD01175	Rat neurite growth
C	17	503.2	13.5	1758	22	AAF32725	Human secreted pro
	18	497.4	13.3	600	22	AAF90323	Human NOGO-C cDNA.
	19	497.4	13.3	770	21	AAA72983	Human NSPH encodin
	20	497.4	13.3	799	19	AAV23695	Human NSPLP protei
	21	497.4	13.3	1122	21	AAZ56888	Human MAGI polypep
	22	497.4	13.3	1122	22	AAF90325	Human NOGO-B cDNA.
	23	497.4	13.3	1213	20	AAX04379	Human secreted pro
	24	497.4	13.3	1216	24	ABA05903	Human RTN4B encodi
	25	497.4	13.3	2052	24	ABK90133	DNA encoding human
	26	497.4	13.3	2235	24	ABV94681	Human pancreatic c
	27	497.4	13.3	2240	21	AAC64406	Human Nogo B nucle
	28	495.8	13.3	991	20	AAX97587	Extended human sec
	29	495.8	13.3	1610	21	AAZ36230	cDNA encoding a bo
	30	495.8	13.3	1694	22	AAK94408	Human full-length
	31	483.6	12.9	868	21	AAZ56887	Human MAGI polypep
	32	475	12.7	1798	24	ABK90135	DNA encoding human
	33	468	12.5	1514	24	ABK34580	Human cDNA for nov
	34	391.6	10.5	1683	22	AAD08386	Human secreted pro
	35	375.6	10.0	422	25	ABX43312	Bovine EST associa
	36	374	10.0	422	25	ABX46402	Bovine EST associa
	37	323	8.6	460	20	AAV87027	EST clone BG160.
	38	322.4	8.6	389	25	ABX39989	Bovine EST associa
	39	316.2	8.5	615	22	AAK93939	Human cDNA clone r
	40	302.6	8.1	423	25	ABX43927	Bovine EST associa
	41	299	8.0	562	22	AAK93574	Human cDNA clone r
C	42	278.8	7.5	742	22	AAI96236	Human neuroblastom
	43	266.4	7.1	668	24	ABL89601	Human polynucleoti
	44	258.2	6.9	495	22	AAK92091	Human cDNA 5'-end
	45	253.2	6.8	3202	19	AAX75770	Human neuroendocri

ALIGNMENTS

```
RESULT 1
AAD01173
ID   AAD01173 standard; cDNA; 4684 BP.
XX
AC   AAD01173;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat neurite growth inhibitor Nogo A cDNA.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             253..3744
FT                   /*tag=  a
FT                   /product= "Nogo A"
FT                   /transl_except= (pos:1462..1464, aa:Ile)
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US26160.
XX
PR   06-NOV-1998;   98US-0107446.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
DR   P-PSDB; AAY71310.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic
PT   disorders of the central nervous system and inducing regeneration of
PT   neurons -
XX
PS   Claim 26; Fig 2A; 122pp; English.
XX
CC   The present sequence is a cDNA encoding rat Nogo A protein which is a
CC   potent neural cell growth inhibitor and is free of all central nervous
CC   system (CNS) myelin material with which it is natively associated.
CC   The present sequence was generated by fusing RO18U37-3, R1-3U21 cDNA
CC   sequences isolated from hexanucleotides-primed rat brain stem/spinal cord
CC   library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte
CC   library. Nogo proteins and fragments displaying neurite growth inhibitory
CC   activity are used in the treatment of neoplastic disease of the CNS
```

CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.
XX
SQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 other;

Query Match 100.0%; Score 3739.4; DB 21; Length 4684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60

Qy         61 ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120

Qy        121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACA 180

Qy        181 ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240

Qy        241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300

Qy        301 CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360

Qy        361 GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG 420

Qy        421 CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG 480

Qy        481 CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        481 CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCC 540

Qy        541 GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG 600

Qy        601 CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT 660

Qy        661 CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG 720

Qy        721 CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT 780

Qy        781 TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT 840

Qy        841 TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG 900

Qy        901 CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA 960

Qy        961 CATGGATACCTTGGTAACTTATCAGCAGTGTCATCCTCAGAAGGAACAATTGAAGAAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CATGGATACCTTGGTAACTTATCAGCAGTGTCATCCTCAGAAGGAACAATTGAAGAAACT 1020

Qy       1021 TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT 1080

Qy       1081 TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA 1140

Qy       1141 AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA 1200

Qy       1201 GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT 1260

Qy       1261 AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATG 1320

Qy       1321 TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG 1380
```

```
Qy       1381 GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA 1440

Qy       1441 AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT 1500

Qy       1501 AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC 1560

Qy       1561 TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC 1620

Qy       1621 ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAAATAGAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAAATAGAA 1680

Qy       1681 GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT 1740

Qy       1741 GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT 1800

Qy       1801 GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT 1860

Qy       1861 GAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG 1920

Qy       1921 GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCCATCA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCCATCA 1980

Qy       1981 TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCA 2040

Qy       2041 TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG 2100

Qy       2101 GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCACCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCACCA 2160

Qy       2161 TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG 2220
```

```
Qy       2221 CCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT 2280

Qy       2281 GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA 2340

Qy       2341 GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCA 2400

Qy       2401 CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACA 2460

Qy       2461 CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC 2520

Qy       2521 CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG 2580

Qy       2581 TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG 2640

Qy       2641 ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT 2700

Qy       2701 GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA 2760

Qy       2761 TCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCT 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCT 2820

Qy       2821 AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC 2880

Qy       2881 CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT 2940

Qy       2941 ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA 3000

Qy       3001 TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC 3060

Qy       3061 AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA 3120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA 3120

Qy       3121 GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT 3180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT 3180

Qy       3181 GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA 3240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA 3240

Qy       3241 TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG 3300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG 3300

Qy       3301 GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG 3360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG 3360

Qy       3361 AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG 3420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG 3420

Qy       3421 GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA 3480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA 3480

Qy       3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG 3540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG 3540

Qy       3541 TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG 3600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG 3600

Qy       3601 ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT 3660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT 3660

Qy       3661 CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT 3720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT 3720

Qy       3721 GGATTGAAGCGCAAAGCAGAT 3741
                |||||||||||||||||||||
Db       3721 GGATTGAAGCGCAAAGCAGAT 3741
```

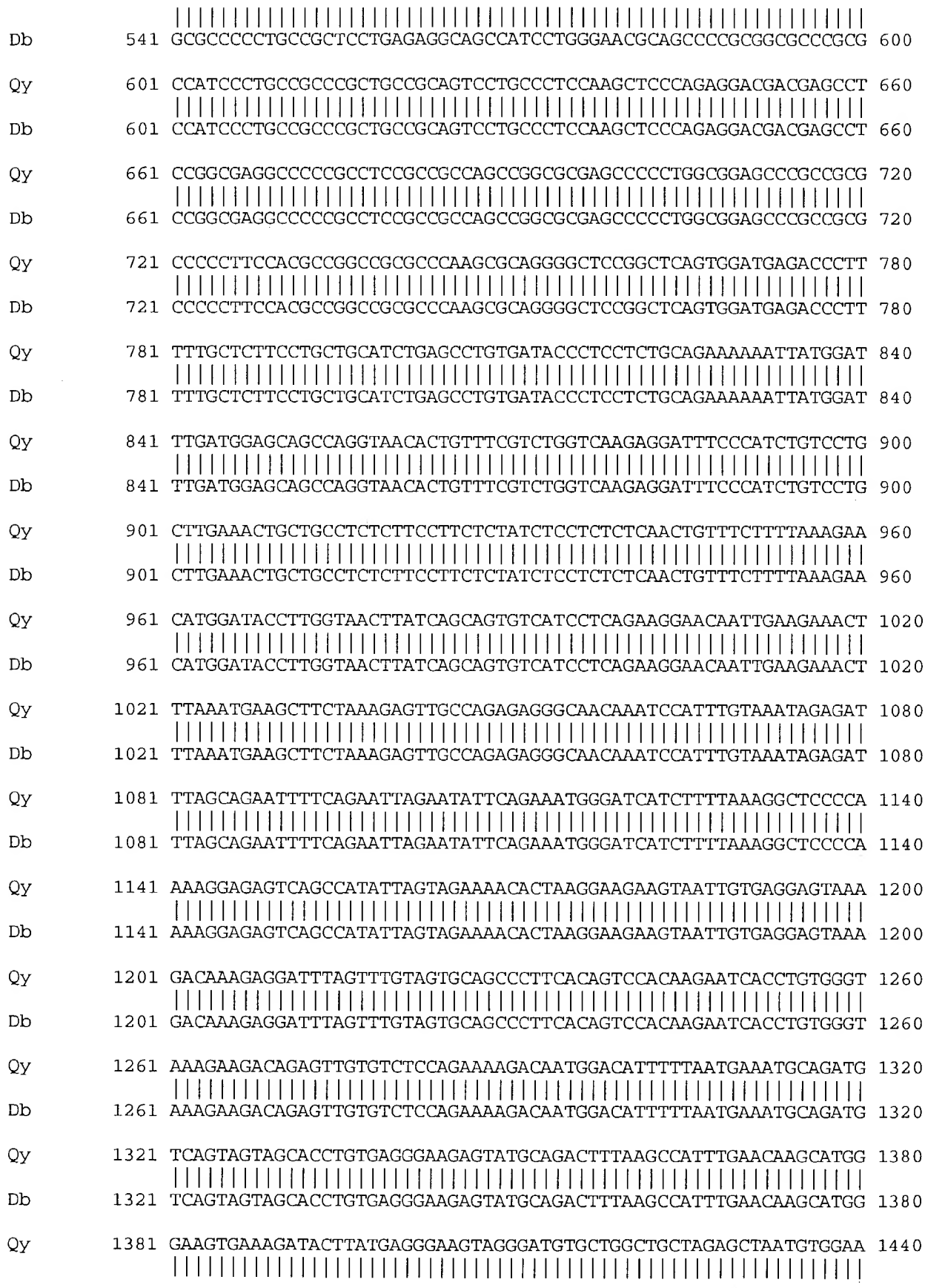
RESULT 2
ABN86600
ID   ABN86600 standard; DNA; 4684 BP.
XX
AC   ABN86600;
XX
DT   05-NOV-2002 (first entry)
XX
DE   Rat neurotransmitter receptor protein Nogo encoding DNA.

XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; gene; ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 253..3744
FT /*tag= a
FT /product= "Nogo-A"
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-0893348.
XX
PR 19-MAY-1998; 98IL-0124500.
PR 21-JUL-1998; 98WO-US14715.
PR 22-DEC-1998; 98US-0218277.
PR 19-MAY-1999; 99US-0314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR P-PSDB; ABB81074, ABB81076, ABB81077.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in
PT the central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -
XX
PS Disclosure; Page 40-44; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease
CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such

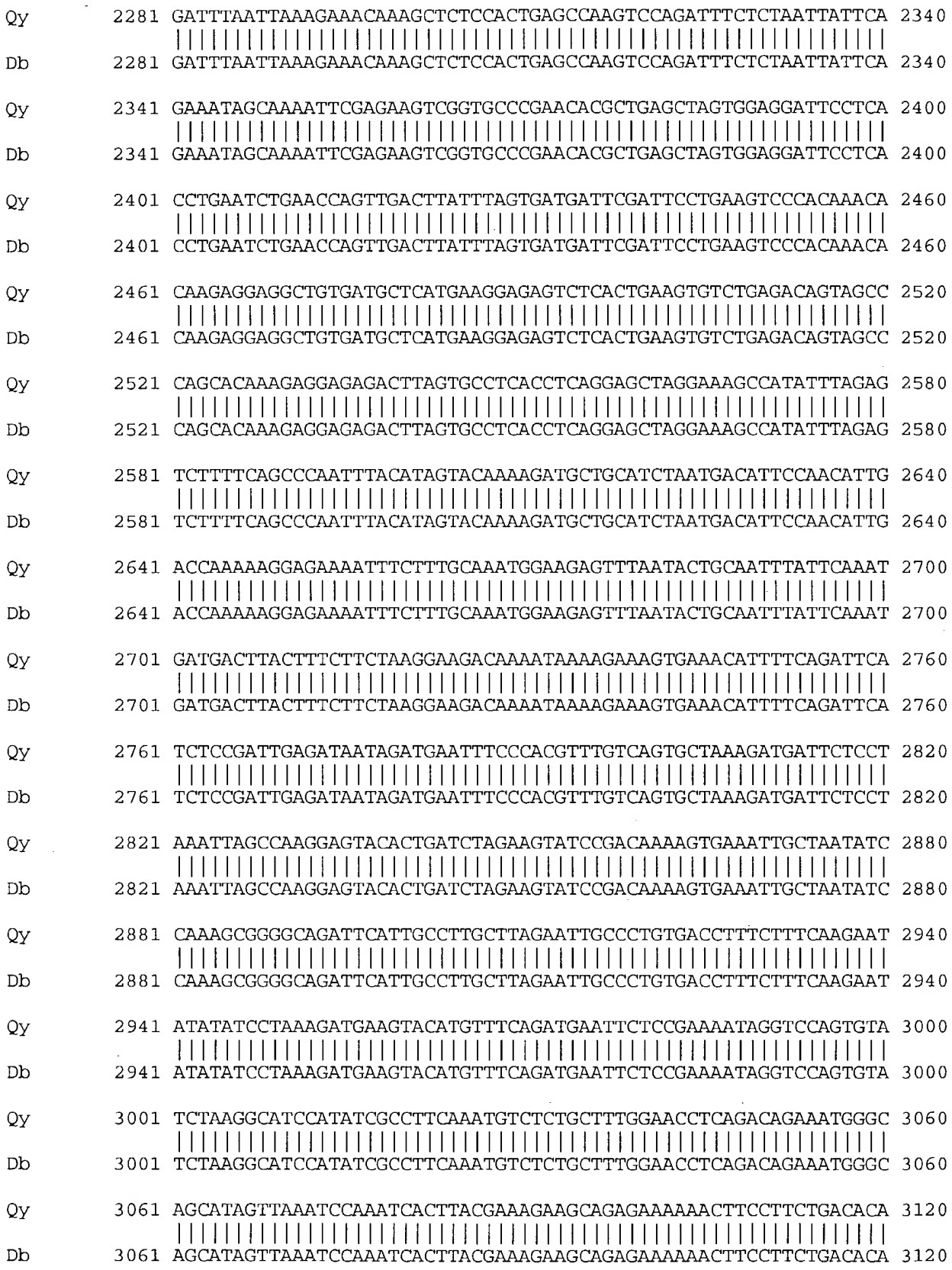
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen.
XX
SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 other;

Query Match 100.0%; Score 3739.4; DB 24; Length 4684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60

Qy         61 ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120

Qy        121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACA 180

Qy        181 ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240

Qy        241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300

Qy        301 CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360

Qy        361 GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG 420

Qy        421 CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG 480

Qy        481 CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCC 540

Qy        541 GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG 600
```



```
Db       1381 GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA 1440

Qy       1441 AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT 1500

Qy       1501 AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC 1560

Qy       1561 TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC 1620

Qy       1621 ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA 1680

Qy       1681 GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT 1740

Qy       1741 GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT 1800

Qy       1801 GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT 1860

Qy       1861 GAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG 1920

Qy       1921 GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCCATCA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTTTGCCCATCA 1980

Qy       1981 TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCA 2040

Qy       2041 TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG 2100

Qy       2101 GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCCACCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCCACCA 2160

Qy       2161 TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG 2220

Qy       2221 CCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT 2280
```

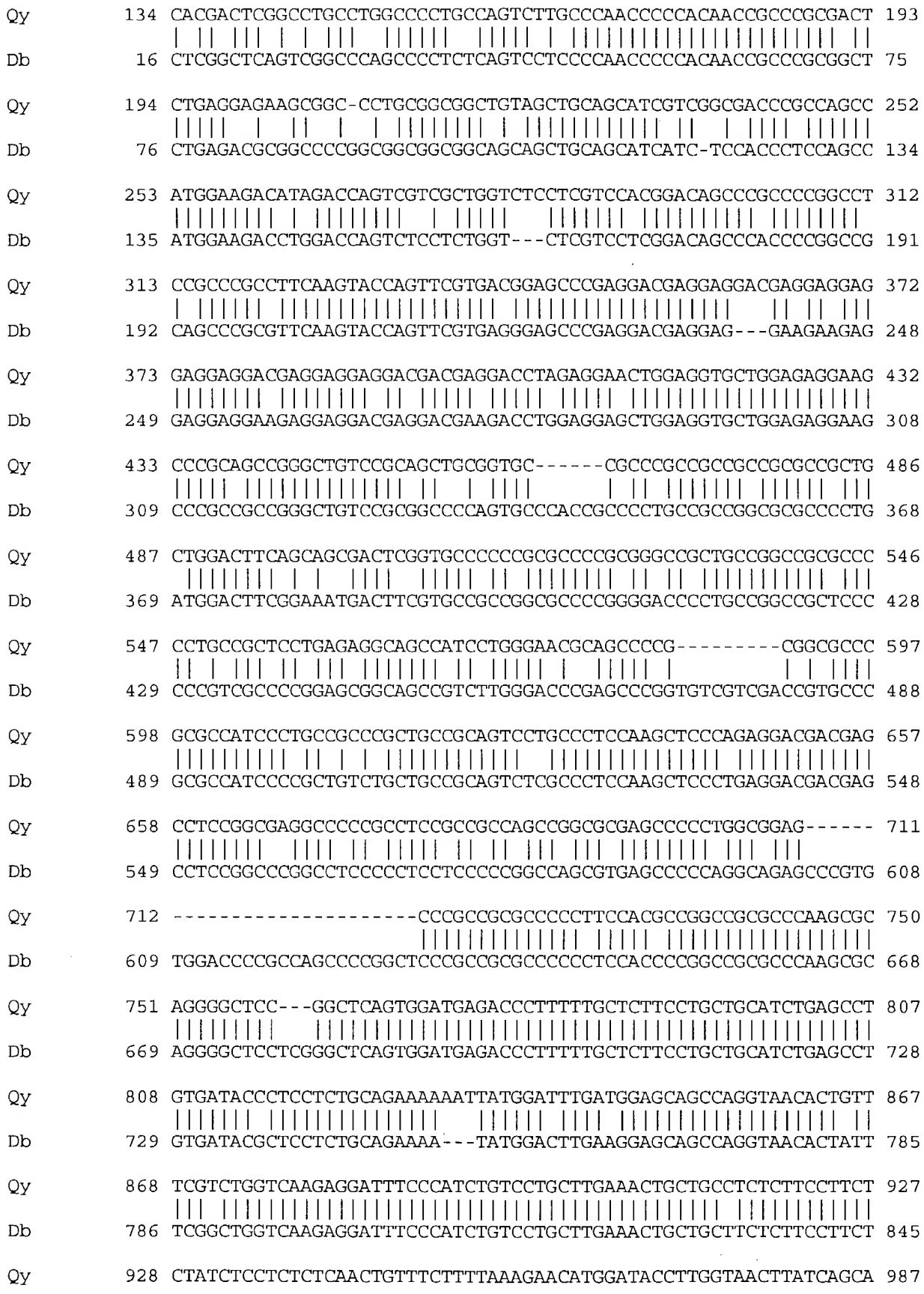


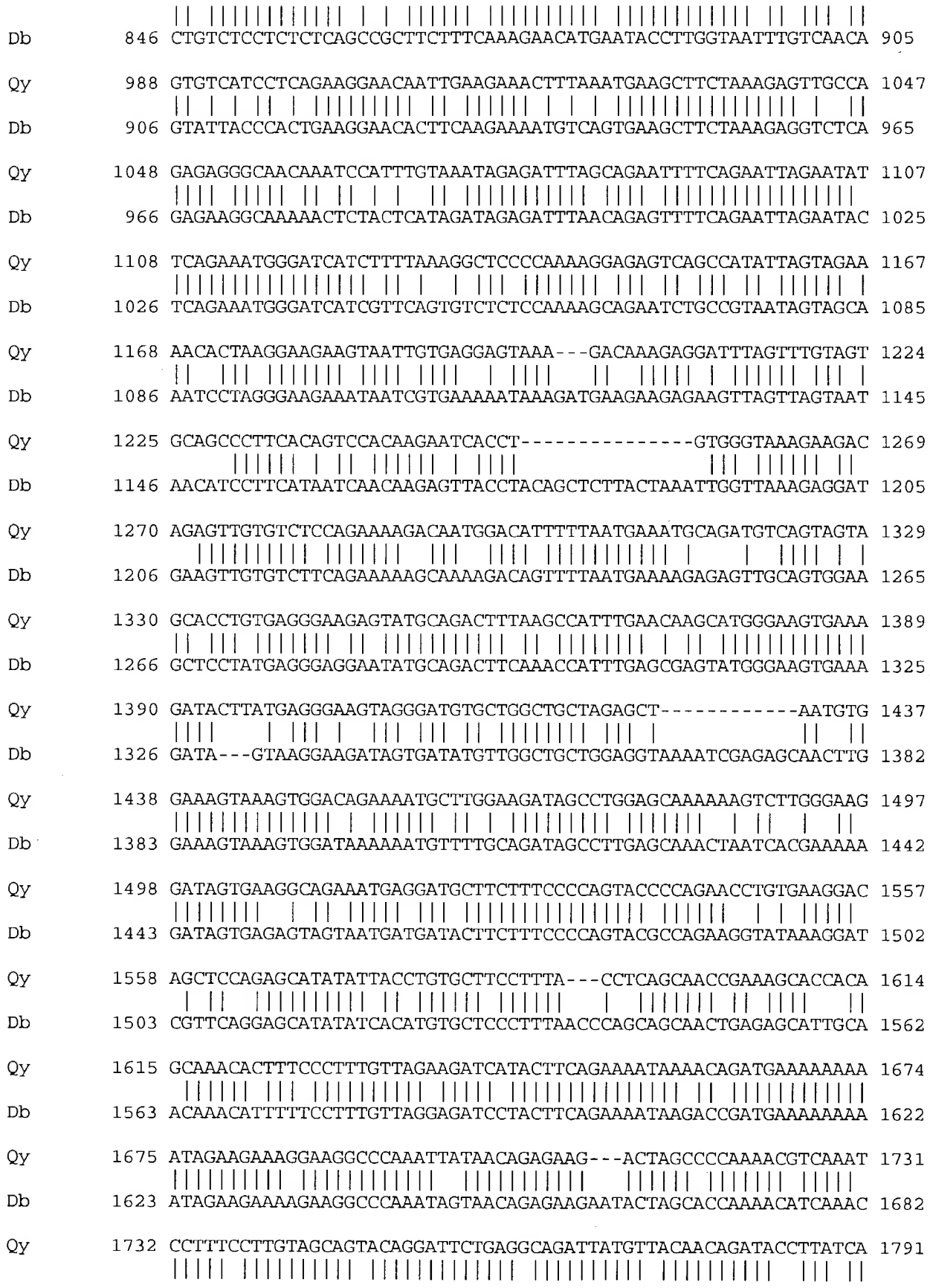
```
Qy       3121 GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT 3180

Qy       3181 GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA 3240

Qy       3241 TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG 3300

Qy       3301 GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG 3360

Qy       3361 AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG 3420

Qy       3421 GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA 3480

Qy       3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG 3540

Qy       3541 TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG 3600

Qy       3601 ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT 3660

Qy       3661 CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT 3720

Qy       3721 GGATTGAAGCGCAAAGCAGAT 3741
             |||||||||||||||||||||
Db       3721 GGATTGAAGCGCAAAGCAGAT 3741
```

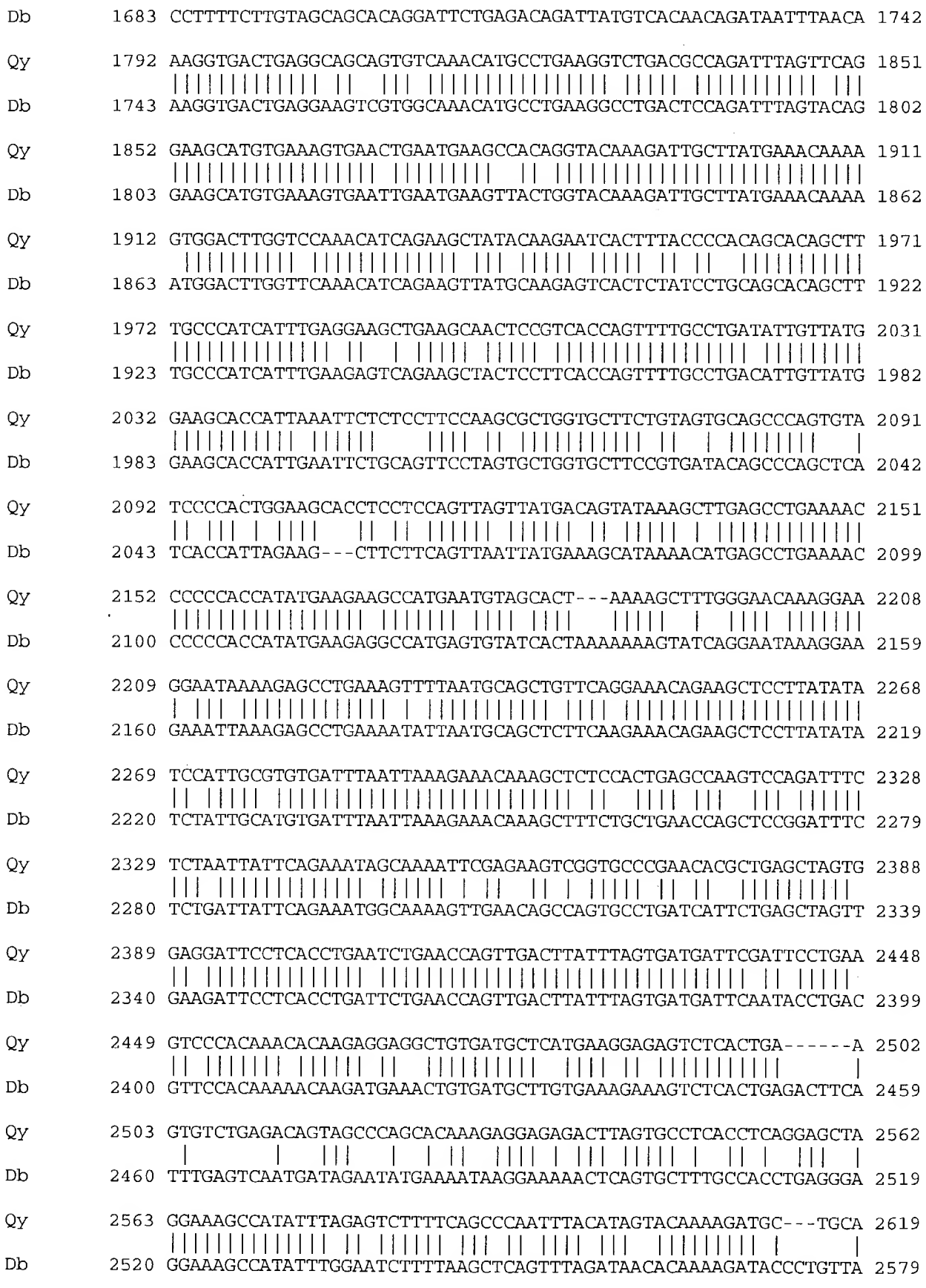
RESULT 3
AAS09453
ID AAS09453 standard; cDNA; 4053 BP.
XX
AC AAS09453;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human cDNA encoding the Nogo protein.
XX
KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

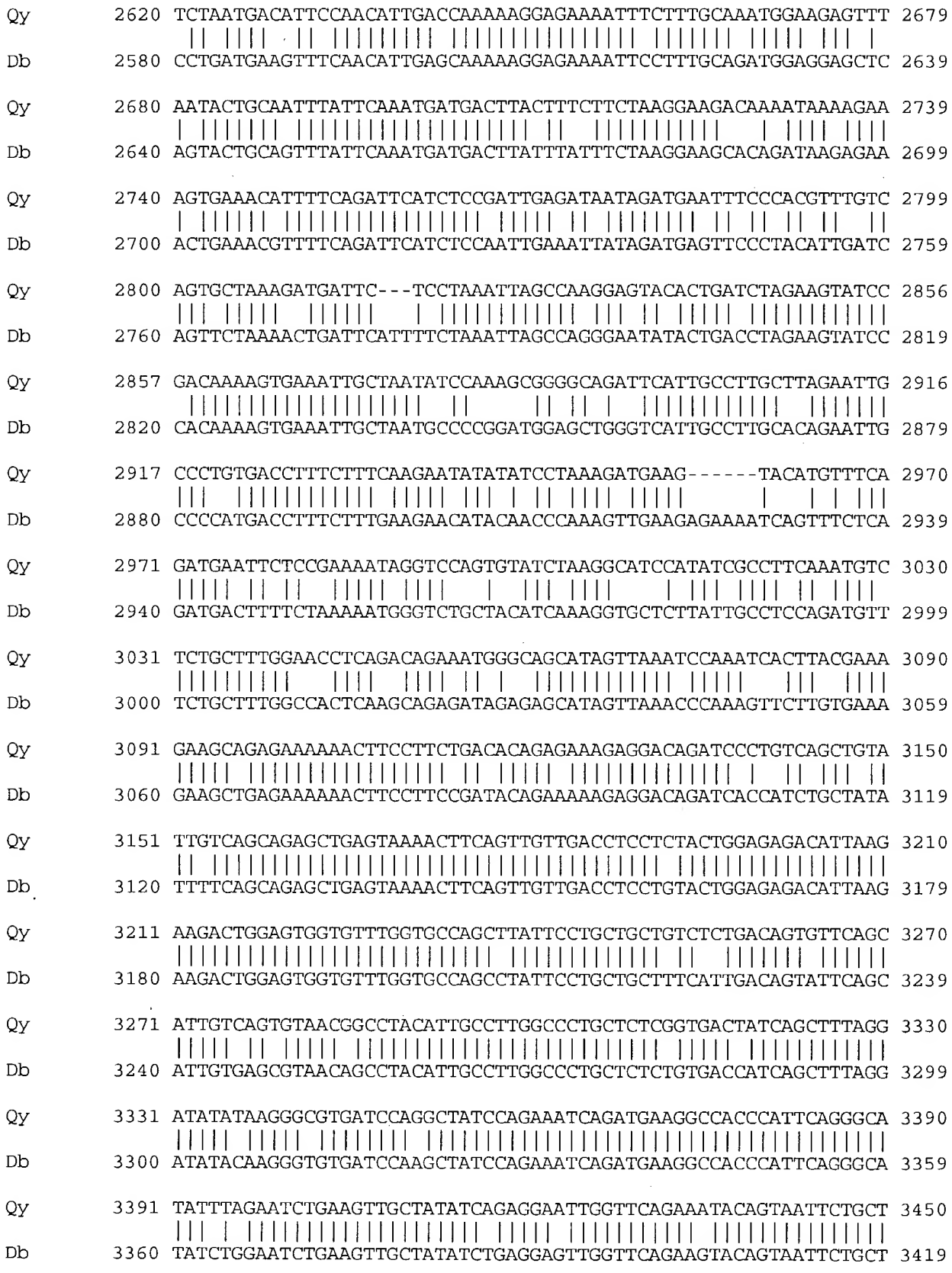
KW demyelinating disease; multiple sclerosis; monophasis demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease; AB020693; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 135..3713
FT /*tag= a
FT /product= "Nogo protein"
XX
PN WO200151520-A2.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US01041.
XX
PR 12-JAN-2000; 2000US-0175707.
PR 26-MAY-2000; 2000US-0207366.
PR 29-SEP-2000; 2000US-0236378.
XX
PA (UYYA) UNIV YALE.
XX
PI Strittmatter SM;
XX
DR WPI; 2001-442138/47.
DR P-PSDB; AAU09453.
XX
PT Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders -
XX
PS Example 1; Page 95-100; 109pp; English.
XX
CC The sequence (Genbank accession number AB0202693) encodes the human Nogo
CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention
CC relates to the use of the nogo receptor, nogo protein, their nucleic
CC acids, vectors expressing them and antibodies against them, to isolate
CC agents which block nogo receptor mediated axonal growth. The agent is
CC useful for treating a central nervous system disorder which is a result
CC of cranial or cerebral trauma, spinal cord injury, stroke or a
CC demyelinating disease selected from multiple sclerosis, monophasis
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,
CC adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
CC viral infection and Krabbe's disease.
XX
SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 other;

Query Match 62.6%; Score 2343.6; DB 22; Length 4053;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;









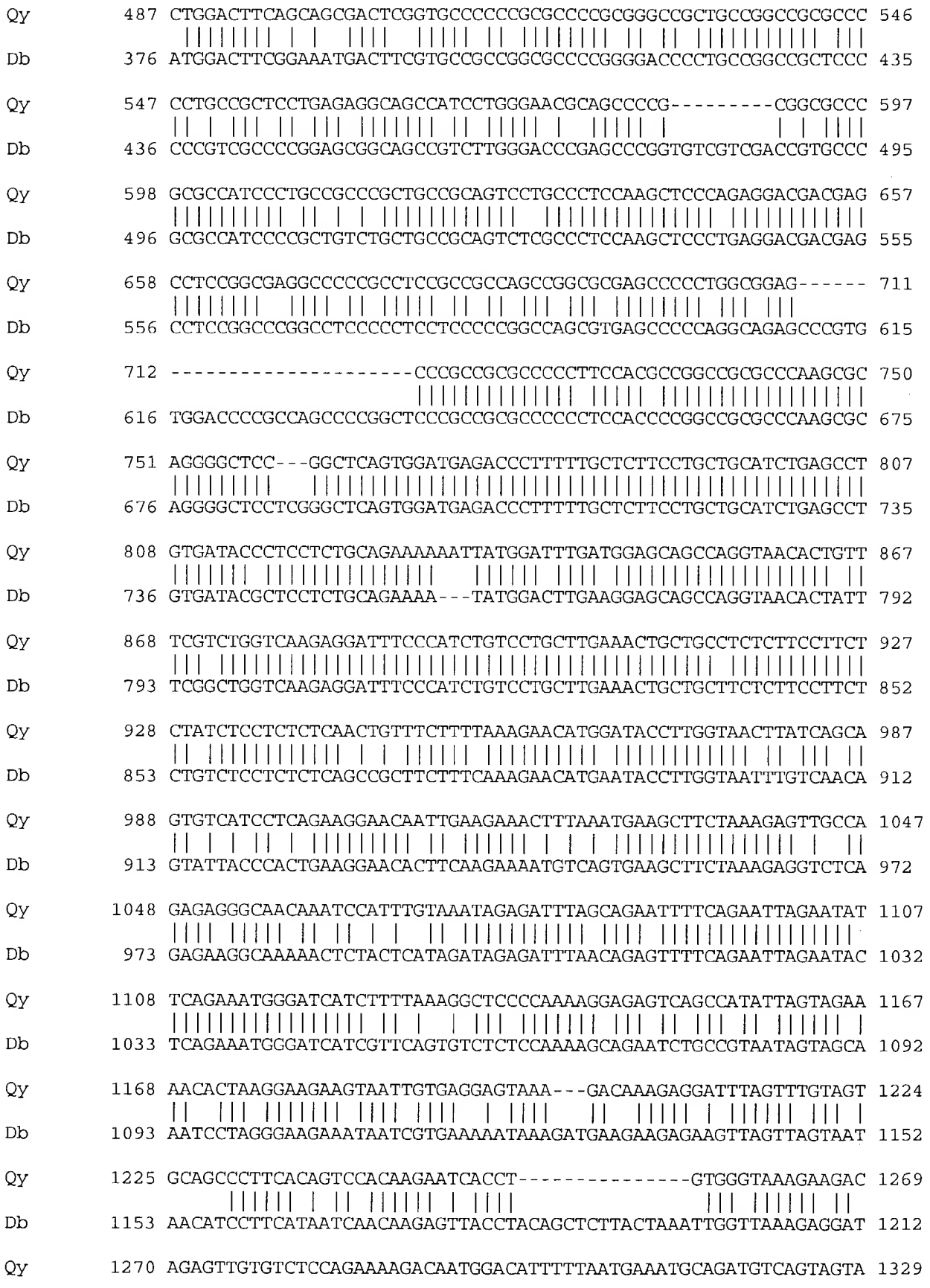
```
Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
             ||||||||||||||| |||| ||||| ||||| ||||| || ||||||||||||||||||
Db       3420 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3479

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
             |||||||| ||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db       3480 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3539

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
             |||||||||||||||||||||| ||||| || |||||||||||| ||||||||||||||
Db       3540 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3599

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
             |||||||||||||  ||||||||||||||||||||||||||| |||| |||||| |||
Db       3600 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3659

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
             || ||||| ||||||||||||||||||||||||||||||||||||||||| ||
Db       3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709
```

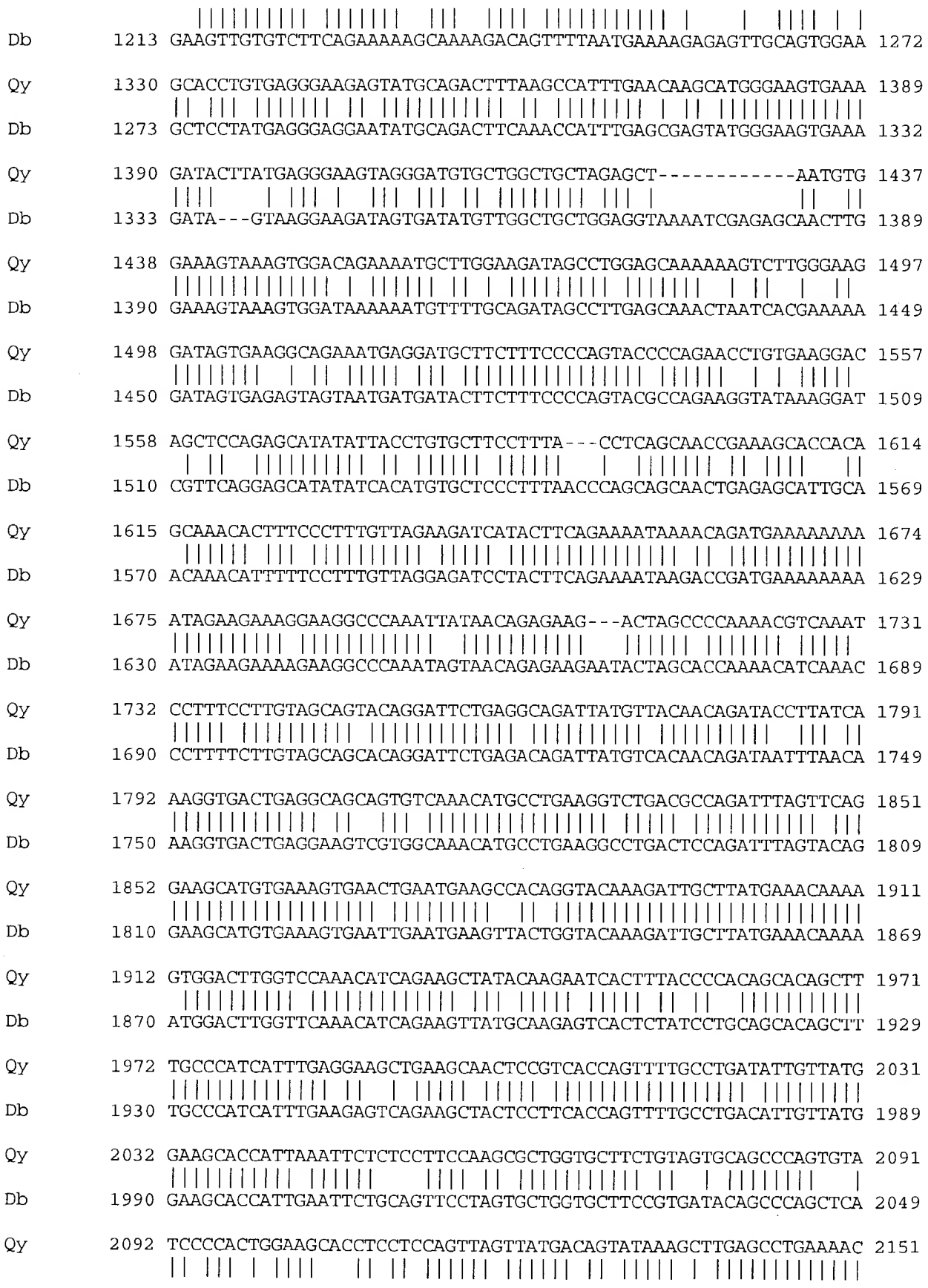
```
RESULT 4
ABV94680
ID   ABV94680 standard; cDNA; 4632 BP.
XX
AC   ABV94680;
XX
DT   14-JAN-2003  (first entry)
XX
DE   Human pancreatic cancer expressed cDNA SEQ ID NO 53.
XX
KW   Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW   cytostatic; tumour; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200260317-A2.
XX
PD   08-AUG-2002.
XX
PF   30-JAN-2002; 2002WO-US02781.
XX
PR   30-JAN-2001; 2001US-265305P.
PR   31-JAN-2001; 2001US-265682P.
PR   09-FEB-2001; 2001US-267568P.
PR   21-MAR-2001; 2001US-278651P.
PR   28-APR-2001; 2001US-287112P.
PR   16-MAY-2001; 2001US-291631P.
PR   12-JUL-2001; 2001US-305484P.
PR   20-AUG-2001; 2001US-313999P.
PR   27-NOV-2001; 2001US-333626P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Benson DR,  Kalos MD,  Lodes MJ,  Persing DH,  Hepler WT,  Jiang Y;
XX
DR   WPI; 2002-627435/67.
```

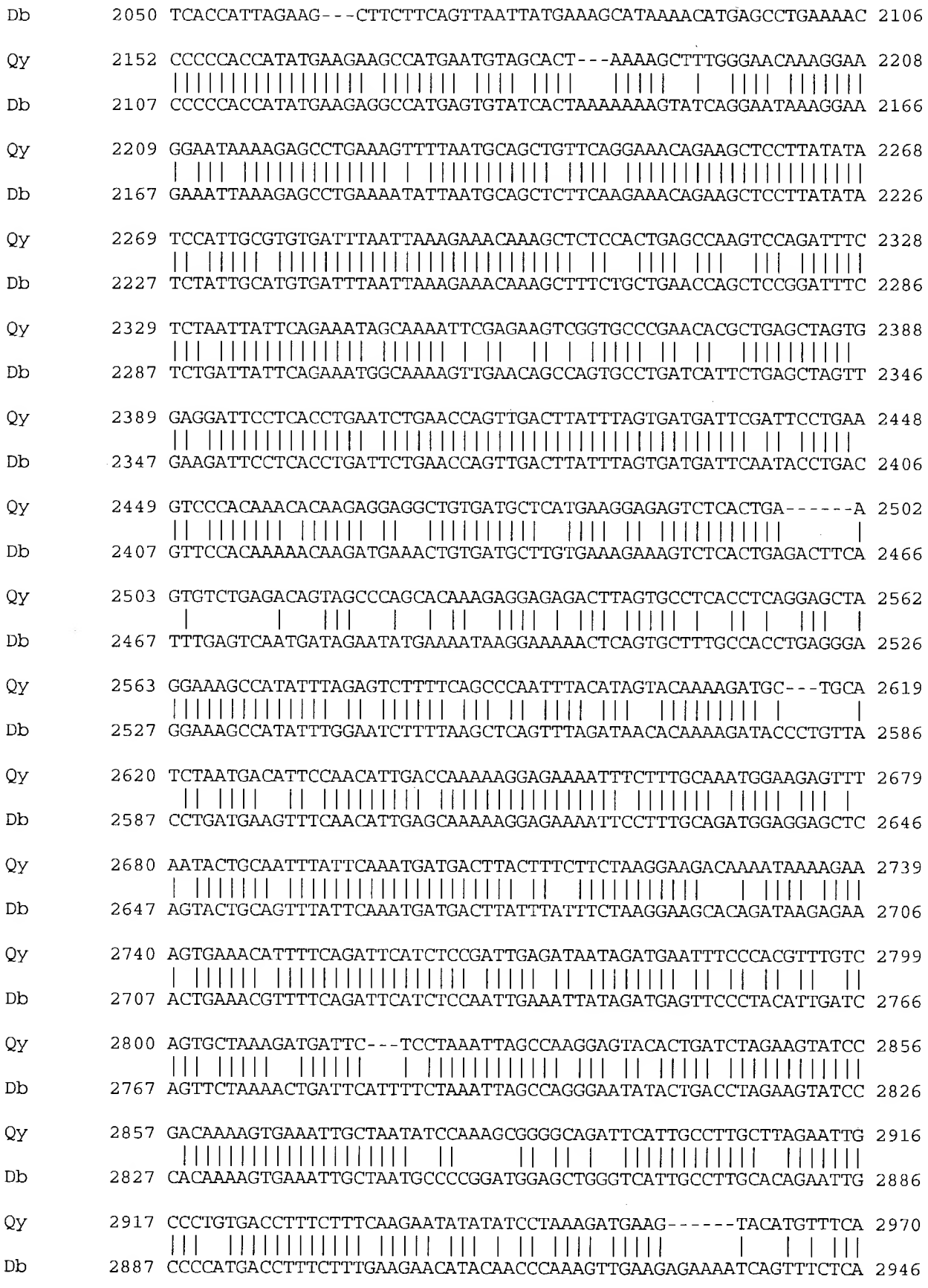
DR P-PSDB; ABP68600.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful
PT for diagnosing, preventing and/or treating cancer, particularly
PT pancreatic cancer -
XX
PS Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
CC (b) complements of (a); (c) sequences consisting of at least 20
CC contiguous residues of (a); (d) sequences that hybridize to (a), under
CC moderately stringent conditions; (e) sequences having at least 75% or 90%
CC identity to (a); or (f) degenerate variants of (a). Polypeptides
CC (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to
CC detect cancer in a patient and compositions comprising polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations and
CC antigen presenting cells expressing the polypeptide are useful in
CC treating pancreatic cancer and stimulating an immune response. The
CC polynucleotides can be used as probes or primers for nucleic acid
CC hybridisation, in the design and preparation of ribozyme molecules for
CC inhibiting expression of the tumour polypeptides and proteins in the
CC tumour cells, in vaccines and for gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 other;

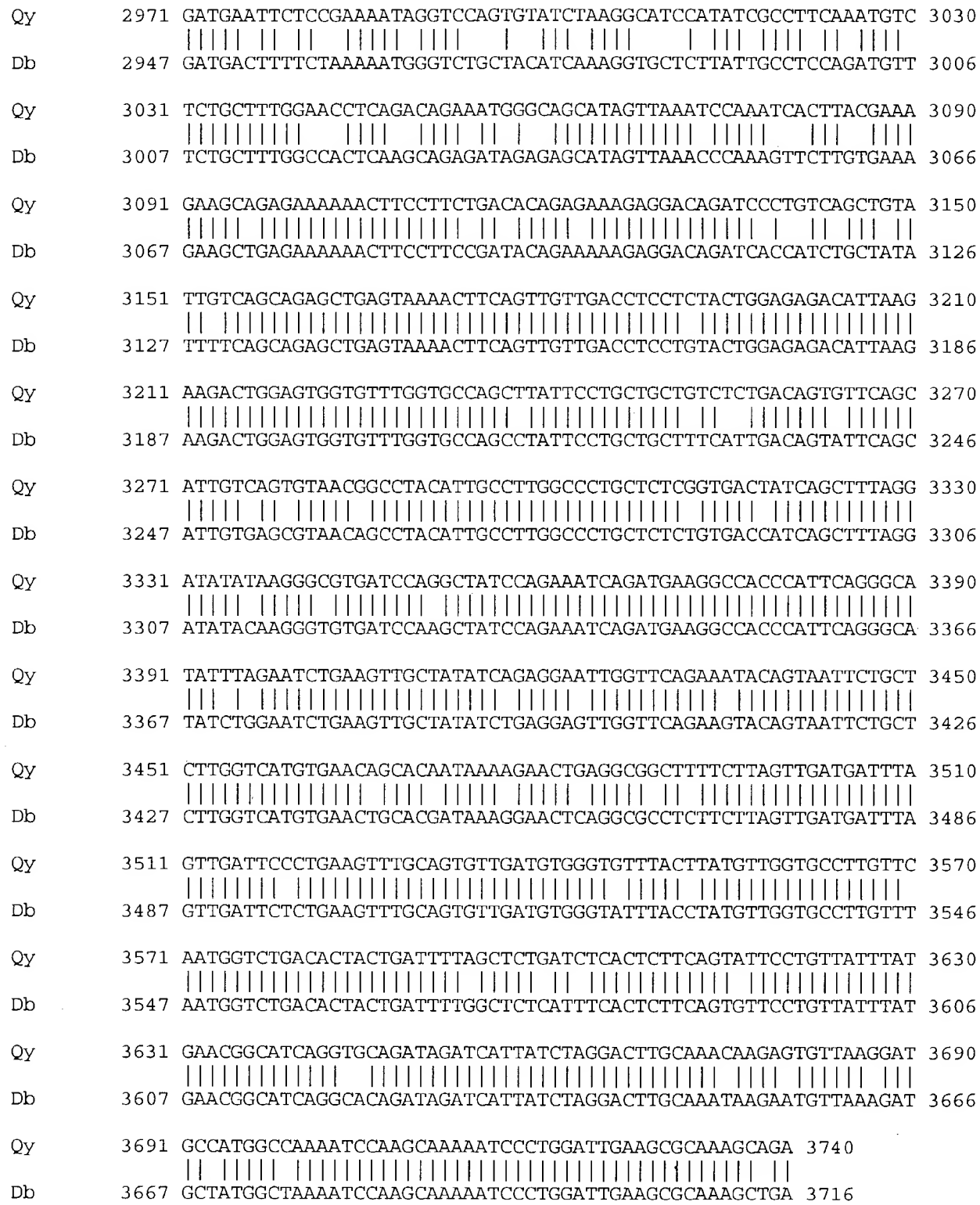
Query Match 62.6%; Score 2343.6; DB 24; Length 4632;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

```
Qy        134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
              | || ||| | | |||  ||||||  ||||| | ||||||||||||||||||||||| ||
Db         23 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 82

Qy        194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
              |||||  |  ||  |  | |||||||| | |||||||||||| ||  | |||| ||||||
Db         83 CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 141

Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
              ||||||||| | ||||||||  | |||||  ||||||| |||||||||| ||||||||
Db        142 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 198

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| |||||||||||||||||| ||||||||||||||||||   || || |||
Db        199 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 255

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        256 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 315

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486
              ||||| |||||||||||||| ||  | ||||      | || ||||||| |||||| |||
Db        316 CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 375
```









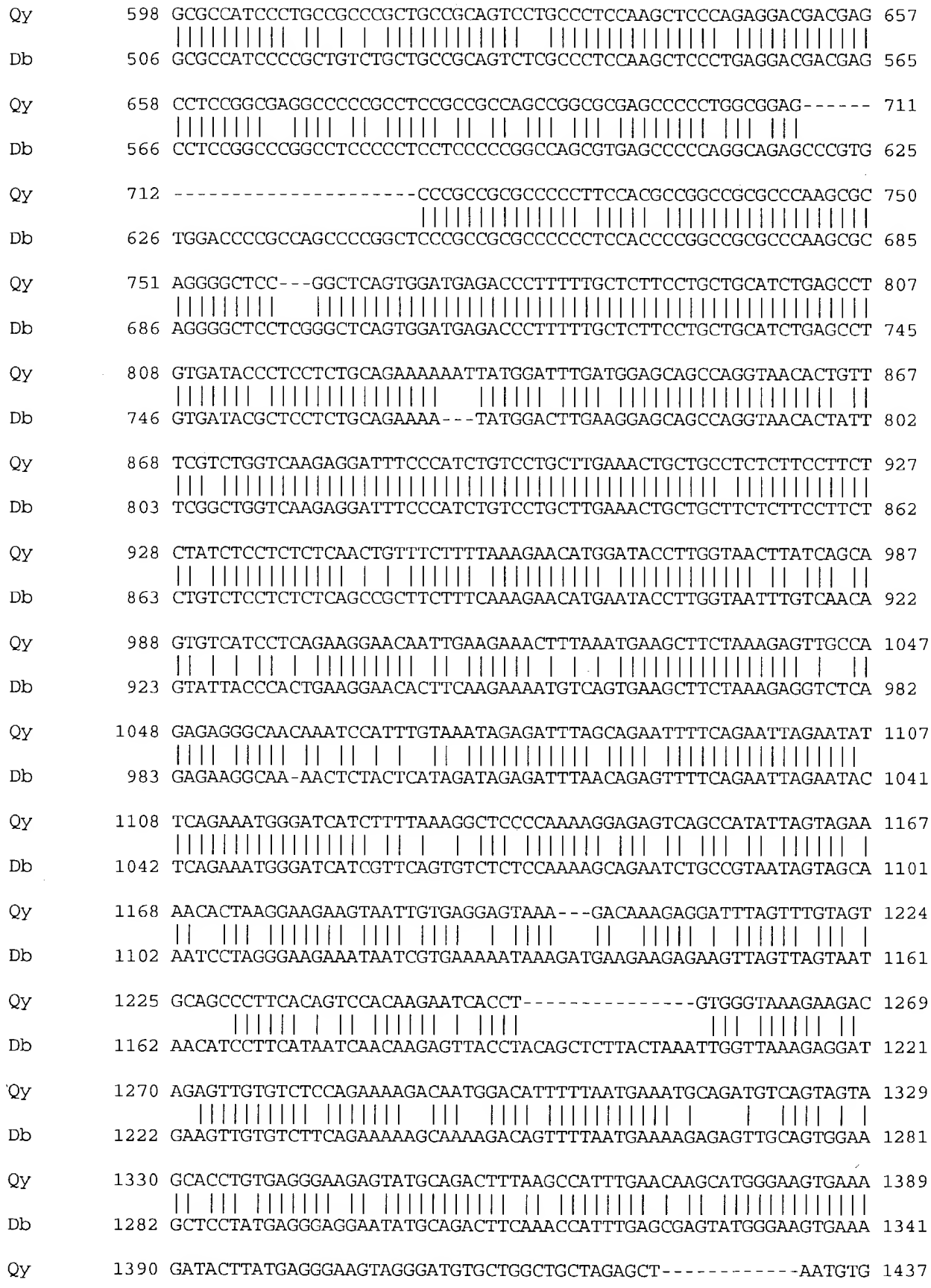
RESULT 5
AAA23454
ID AAA23454 standard; cDNA; 4093 BP.

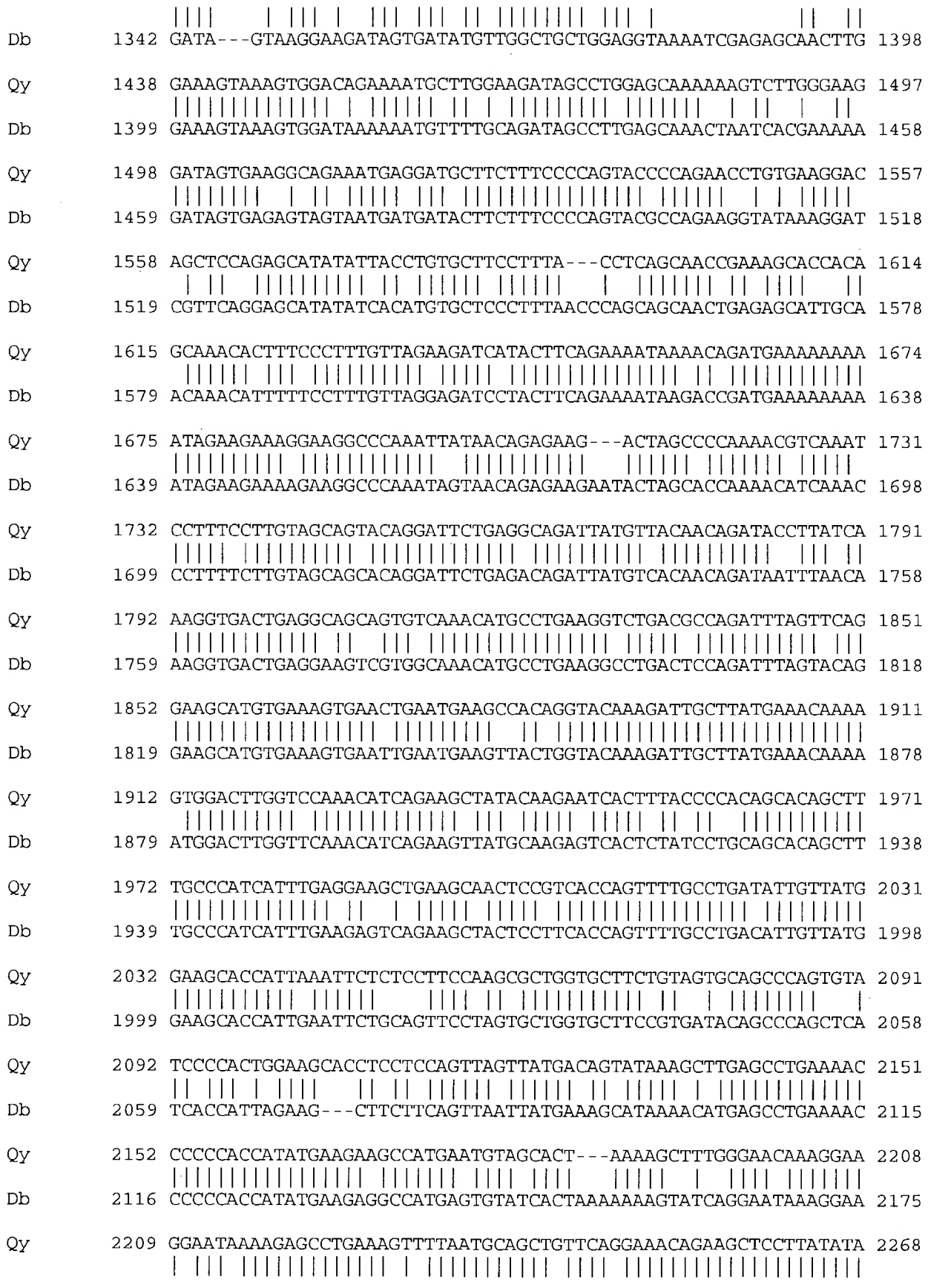
XX
AC AAA23454;
XX
DT 19-JUN-2000 (first entry)
XX
DE cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1048..3729
FT /*tag= a
FT /product= "Human secreted protein vb22_1"
FT CDS 152..1006
FT /*tag= b
FT /product= "Clone vb22_1 ORF2"
XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99WO-US19351.
XX
PR 24-AUG-1998; 98US-0097638.
PR 24-AUG-1998; 98US-0097659.
PR 09-SEP-1998; 98US-0099618.
PR 28-SEP-1998; 98US-0102092.
PR 25-NOV-1998; 98US-0109978.
PR 23-DEC-1998; 98US-0113645.
PR 23-DEC-1998; 98US-0113646.
PR 23-AUG-1999; 99US-0379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
DR P-PSDB; AAY95012, AAY95030.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX
PS Claim 72; Page 321-322; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC invention may exhibit one or more activities selected from the following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;

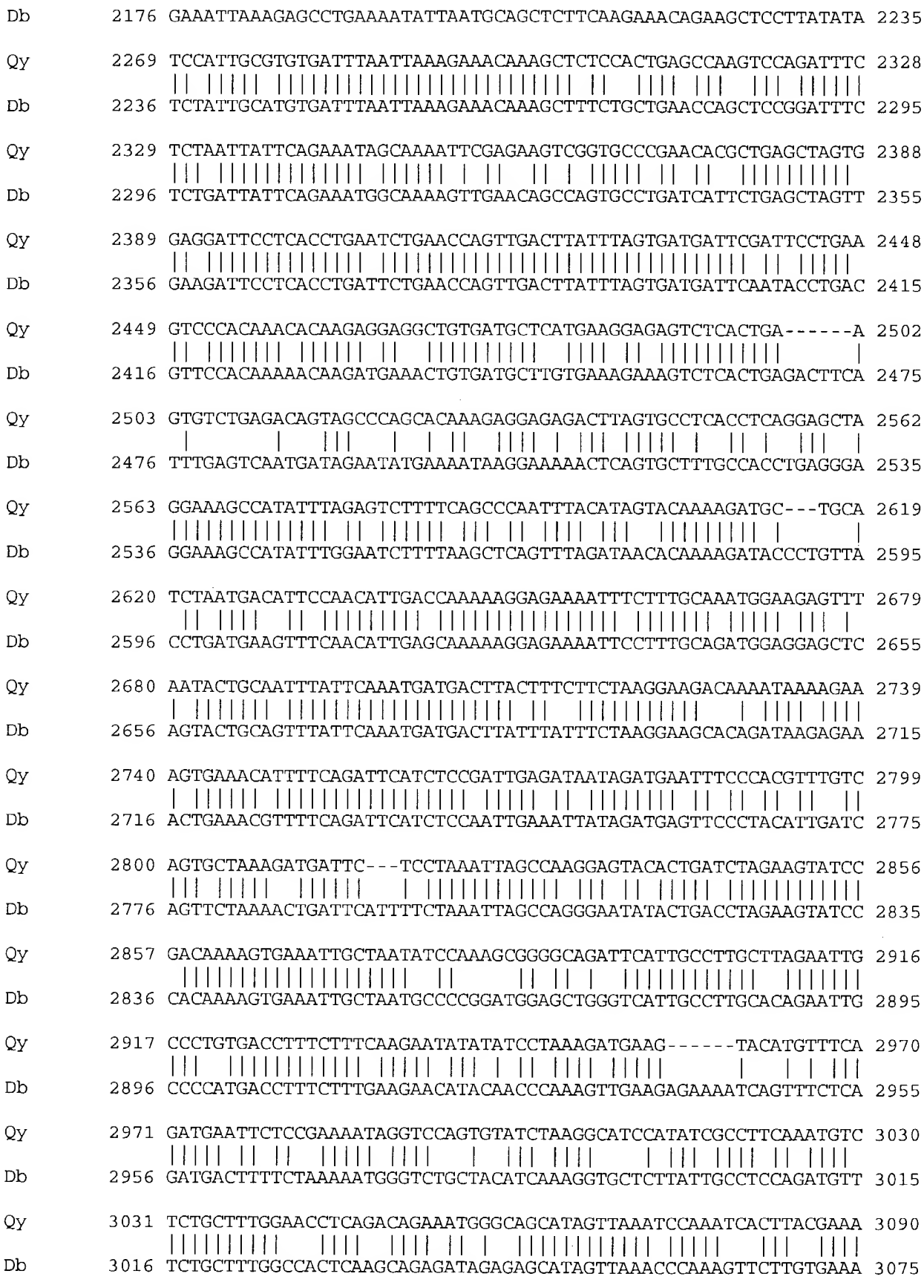
CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy
CC regime. Diseases or conditions that may be treated using the proteins or
CC nucleotides of the invention include autoimmune diseases; genetic
CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
CC fungal and viral infections, especially HIV; multiple sclerosis;
CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
CC insulin dependent diabetes mellitus; and allergic reactions such as
CC asthma and anaemia. They may also be used for treating wounds, burns,
CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease and amyotrophic
CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
CC additionally be useful as contraceptives. Nucleic acid sequences of the
CC invention may be used in chromosome mapping, and as a source of
CC diagnostic primers and probes. The present sequence represents cDNA
CC encoding one of the 40 proteins of the invention.
XX
SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 other;

Query Match 62.4%; Score 2333.2; DB 21; Length 4093;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 573; Indels 120; Gaps 22;

```
Qy        134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
              | || ||| | | |||  ||||||  ||||| | ||||||||||||||||||||||| ||
Db         33 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 92

Qy        194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
              |||||  |  ||  |  | |||||||| | |||||||||||  ||  | |||| ||||||
Db         93 CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 151

Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
              ||||||||| | ||||||||  | |||||  ||||||| |||||||||| ||||||||
Db        152 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 208

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| |||||||||||||||||| |||||||||||||||||   || || |||
Db        209 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 265

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        266 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 325

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486
              ||||| |||||||||||||| ||  | ||||      | || ||||||| |||||| |||
Db        326 CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 385

Qy        487 CTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
               |||||||| | |  |||| ||||| || |||||||| || || |||||||||| |||
Db        386 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 445

Qy        547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG---------CGGCGCCC 597
              || | ||| || ||| ||||||| || ||||| |  ||||| |          | | ||||
Db        446 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 505
```






Db 2176 GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2235
Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTC 2328
Db 2236 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTC 2295
Qy 2329 TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388
Db 2296 TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT 2355
Qy 2389 GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA 2448
Db 2356 GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC 2415
Qy 2449 GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA------A 2502
Db 2416 GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA 2475
Qy 2503 GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA 2562
Db 2476 TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA 2535
Qy 2563 GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA 2619
Db 2536 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA 2595
Qy 2620 TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT 2679
Db 2596 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC 2655
Qy 2680 AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA 2739
Db 2656 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA 2715
Qy 2740 AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC 2799
Db 2716 ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC 2775
Qy 2800 AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC 2856
Db 2776 AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2835
Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG 2916
Db 2836 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTG 2895
Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG------TACATGTTTCA 2970
Db 2896 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2955
Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
Db 2956 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 3015
Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
Db 3016 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 3075

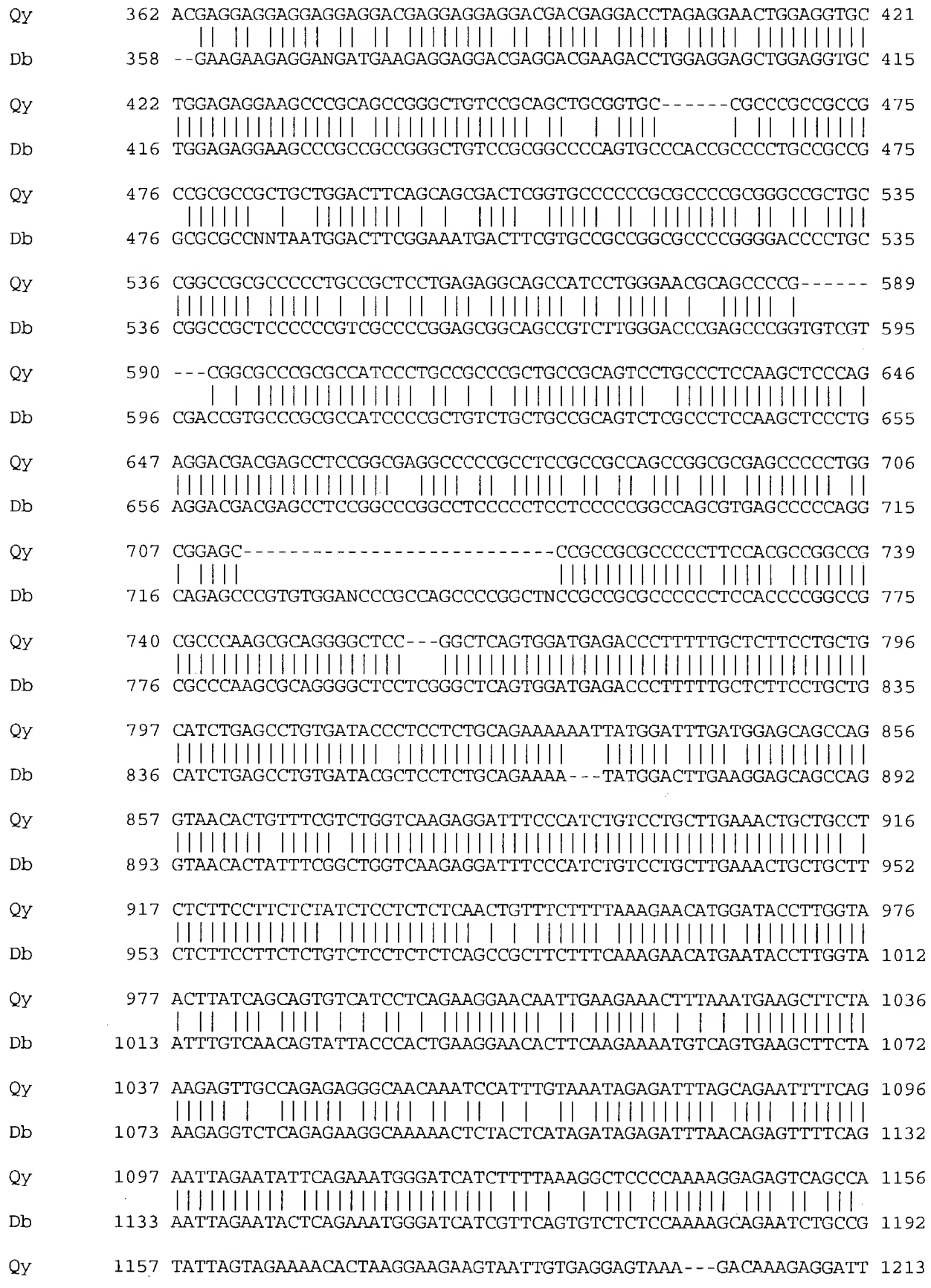
```
Qy       3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150
             ||||| |||||||||||||||| || ||||| |||||||||||||| |  || ||| ||
Db       3076 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 3135

Qy       3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
             || ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       3136 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3195

Qy       3211 AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3270
             |||||||||||||||||||||||||| |||||||||||| ||  ||||||| ||||||
Db       3196 AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3255

Qy       3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
             ||||| || ||||| |||||||||||||||||||||||| ||||| ||||||||||||
Db       3256 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3315

Qy       3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
             ||||| ||||| |||||||| |||||||||||||||||||||||||||||||||||||||
Db       3316 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3375

Qy       3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
             ||| | |||||||||||||||||||| ||||| |||||||||||| ||||||||||||||
Db       3376 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3435

Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
             |||||||||||||||| |||| ||||| ||||| ||||| || ||||||||||||||||||
Db       3436 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3495

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
             |||||||| |||||||||||||||||||||||| ||||| ||||||||||||||||||
Db       3496 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3555

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
             |||||||||||||||||||||||| ||||| || |||||||||||| ||||||||||||||
Db       3556 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3615

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
             |||||||||||||  |||||||||||||||||||||||||||||| |||| |||||| |||
Db       3616 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3675

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
             || ||||| |||||||||||||||||||||||||||||||||||||||||| ||
Db       3676 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3725
```

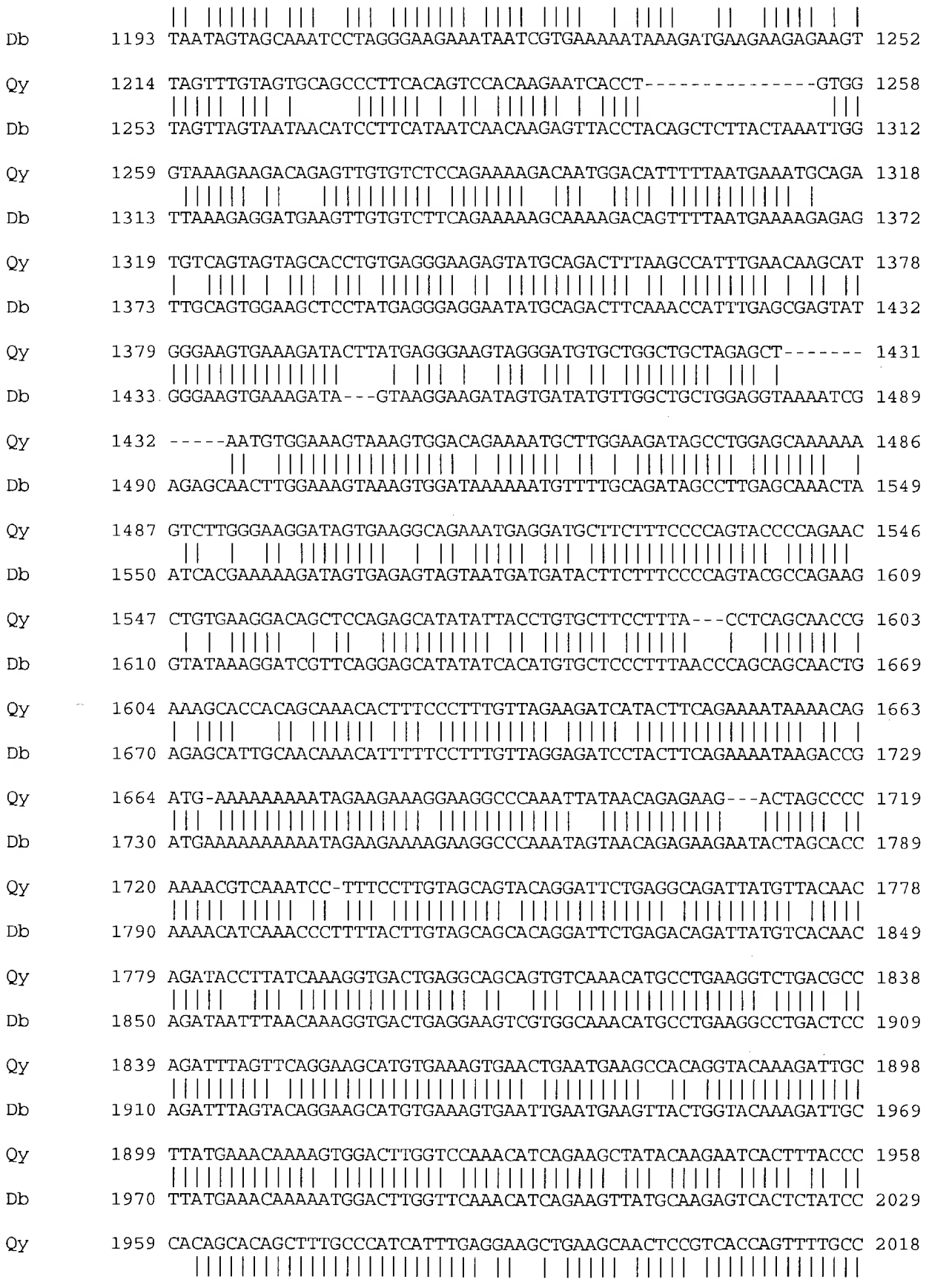
```
RESULT 6
ABS70449
ID   ABS70449 standard; cDNA; 4822 BP.
XX
AC   ABS70449;
XX
DT   27-NOV-2002  (first entry)
XX
DE   Human bone remodelling gene #106.
XX
KW   Bone remodelling; osteoporosis; human; gene; ss.
```

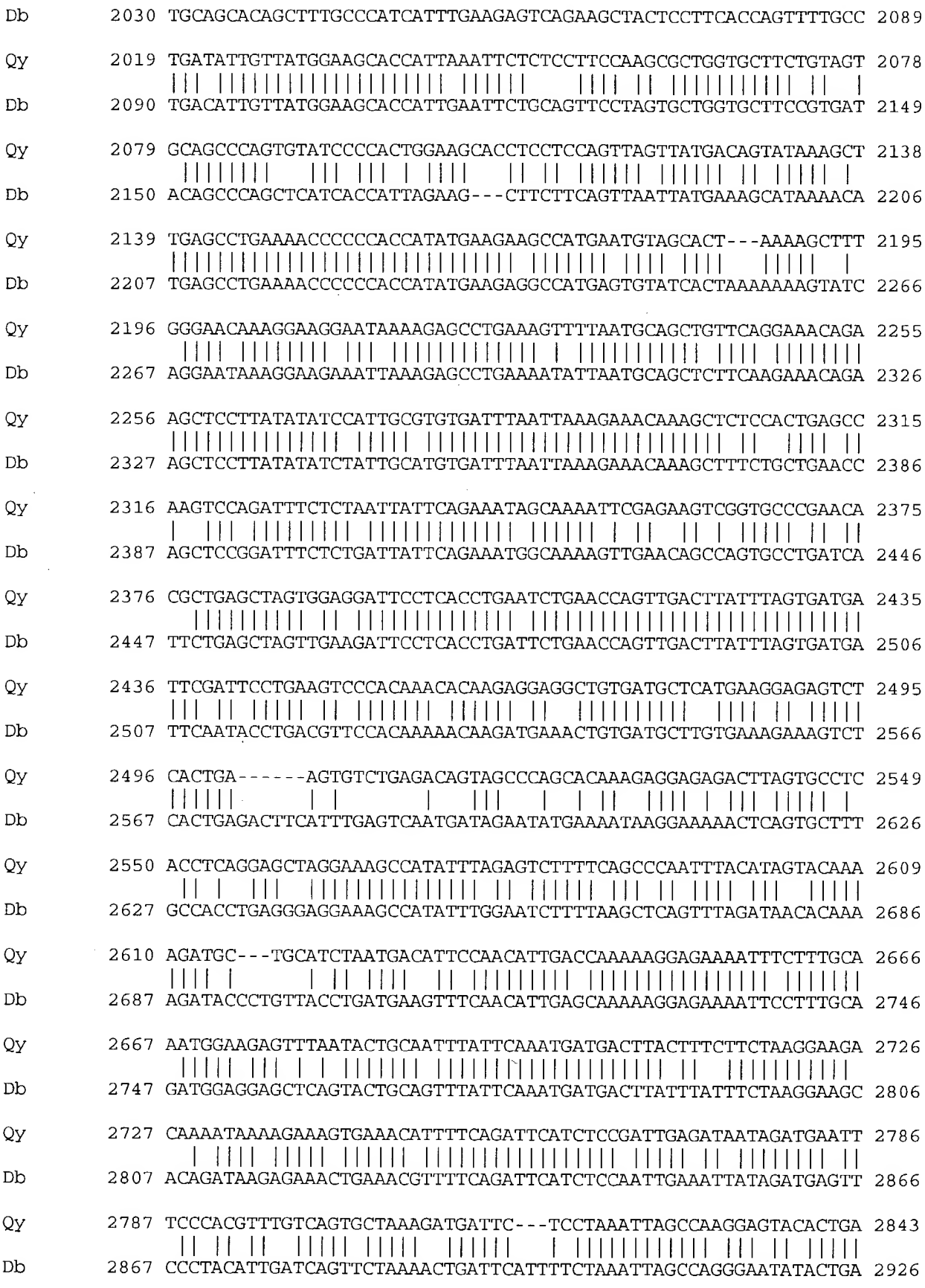
XX
OS Homo sapiens.
XX
PN US6426186-B1.
XX
PD 30-JUL-2002.
XX
PF 18-JAN-2000; 2000US-0484970.
XX
PR 18-JAN-2000; 2000US-0484970.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Volkmuth W, Walker MG;
XX
DR WPI; 2002-673014/72.
XX
PT A combination of polynucleotides which are co-expressed with genes
PT known to be involved in bone remodeling and osteoporosis are useful in
PT an array for the diagnosis of bone remodeling and osteoporosis
PT associated disorders -
XX
PS Claim 1; Column 283-288; 206pp; English.
XX
CC The invention relates to a combination comprising a number of
CC substantially purified and isolated polynucleotides which are
CC co-expressed with genes known to be involved in bone remodelling and
CC osteoporosis. The invention is used to diagnose disorders associated
CC with bone remodelling or osteoporosis. ABS70344-ABS70512 represent
CC human bone remodelling genes of the invention.
XX
SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 15 other;

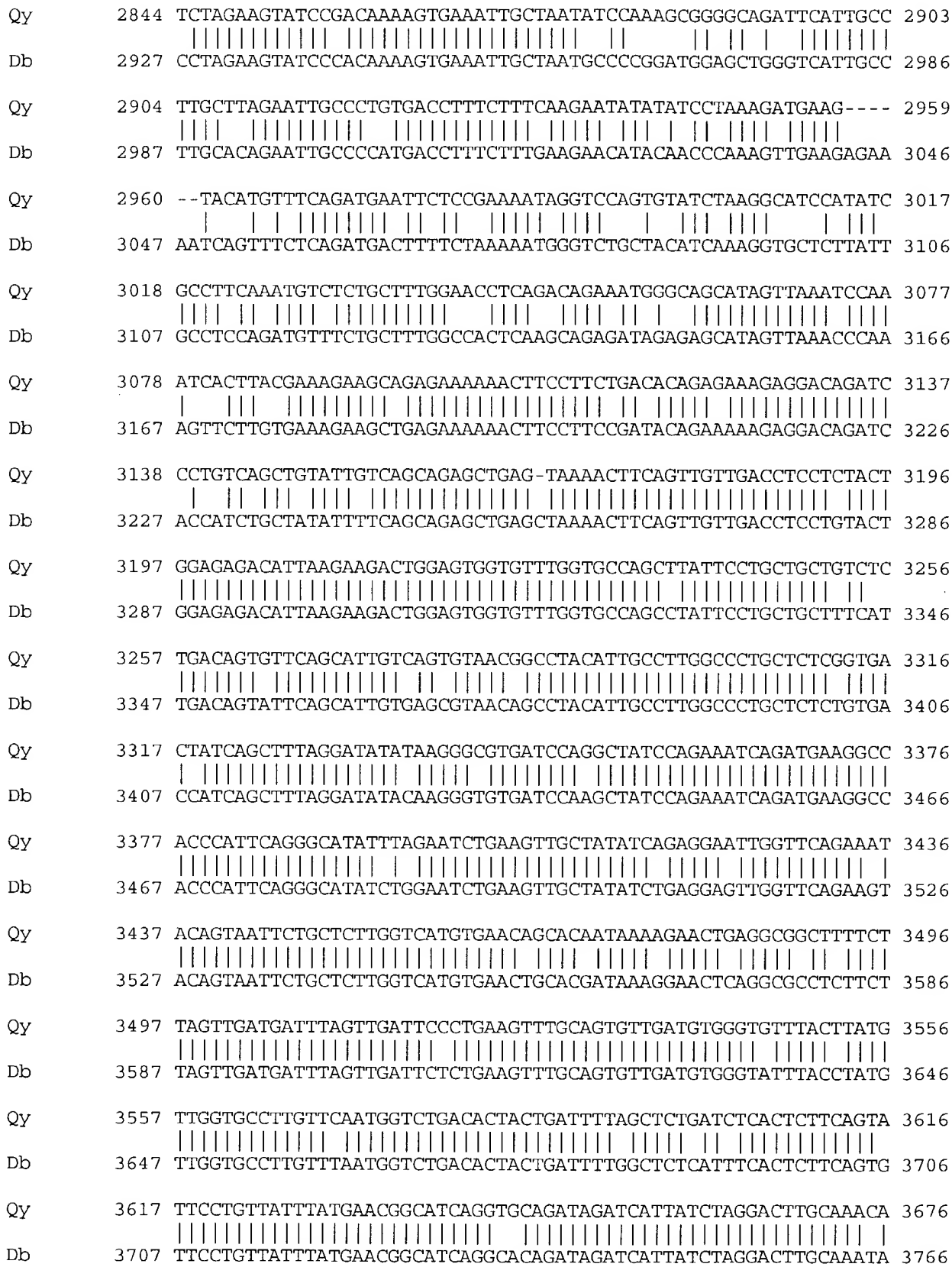
Query Match 62.1%; Score 2323.8; DB 24; Length 4822;
Best Local Similarity 80.9%; Pred. No. 0;
Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;

```
Qy          63 CGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCG 122
               | || |||||| || |||||||||||||||||||||||||||| || | | |||| | |||
Db          78 CNCGGAGGCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCG 137

Qy         123 GCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAAC 182
               |||| |               | |||  ||||||  ||||| | ||||||||||||||||
Db         138 GCTCAGT---------------CGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAAC 182

Qy         183 CGCCCGCGACTCTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCG 241
               |||||||| |||||||  |  ||  |    |||||||| | |||||||||||| ||  |
Db         183 CGCCCGCGGCTCTGAGACGCGGCCCCGGNGGCGGCGGCAGCAGCTGCAGCATCATC-TCC 241

Qy         242 ACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCC 301
               |||| |||||||||||||| | ||||||||  | |||||   ||||||| |||||||||
Db         242 ACCCTCCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCC 298

Qy         302 CGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGG 361
               | |||||||| | |||||| |||||||||||||||||| ||||||||||||||||||
Db         299 CACCCCGGCCGCAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG- 357
```









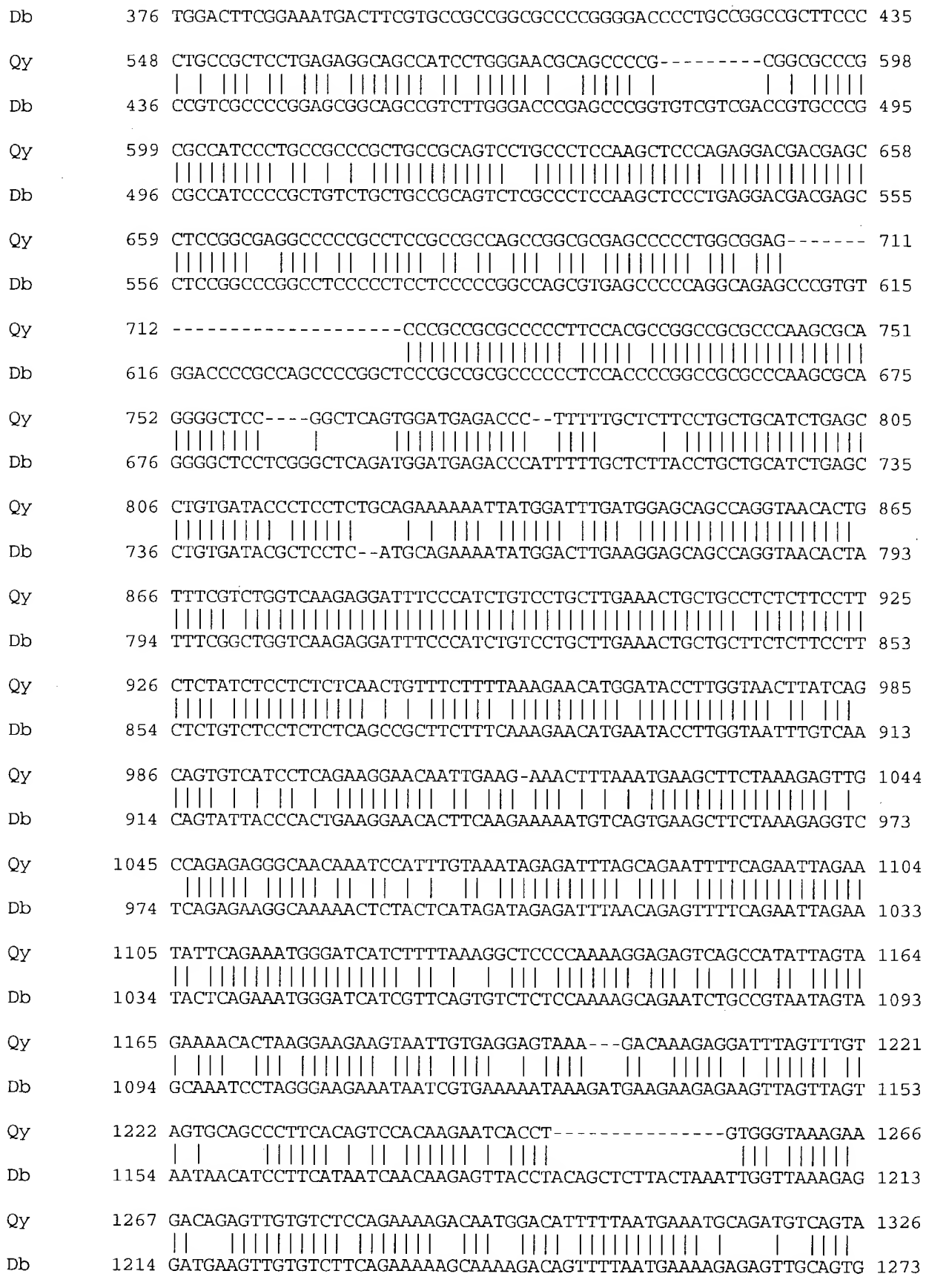
```
Qy       3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736
             ||| |||||| ||||| ||||| ||||||||||||||||||||||||||||||||||||
Db       3767 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3826

Qy       3737 CAGA 3740
             | ||
Db       3827 CTGA 3830
```

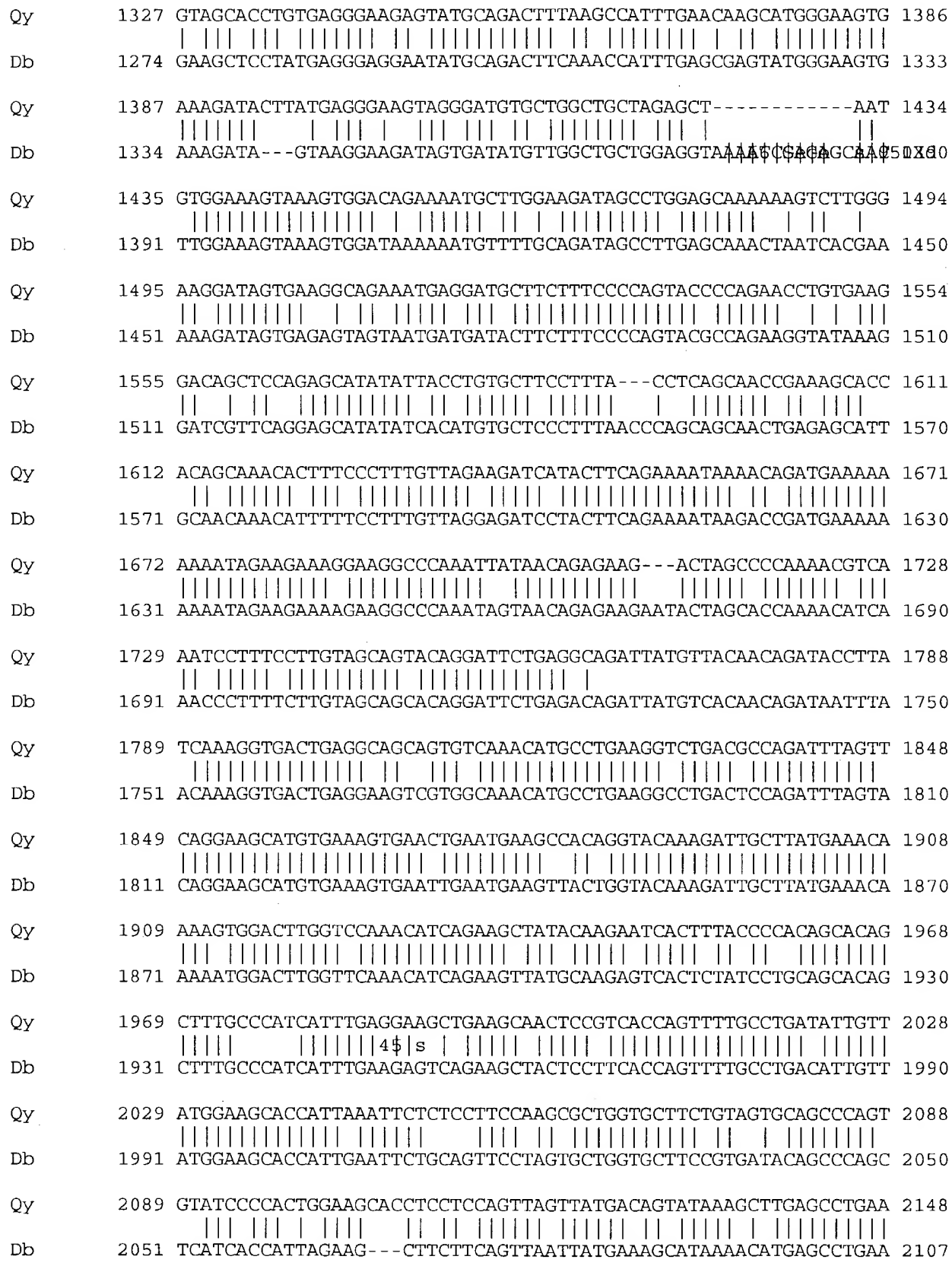
RESULT 7
ABX34563
ID ABX34563 standard; cDNA; 4698 BP.
XX
AC ABX34563;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human mddt cDNA SEQ ID 124.
XX
KW MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW psoriasis; hepatitis; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200279449-A2.
XX
PD 10-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US09944.
XX
PR 28-MAR-2001; 2001US-279619P.
PR 29-MAR-2001; 2001US-280067P.
PR 29-MAR-2001; 2001US-280068P.
PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.
PR 20-JUN-2001; 2001US-300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR P-PSDB; ABU11573.
XX

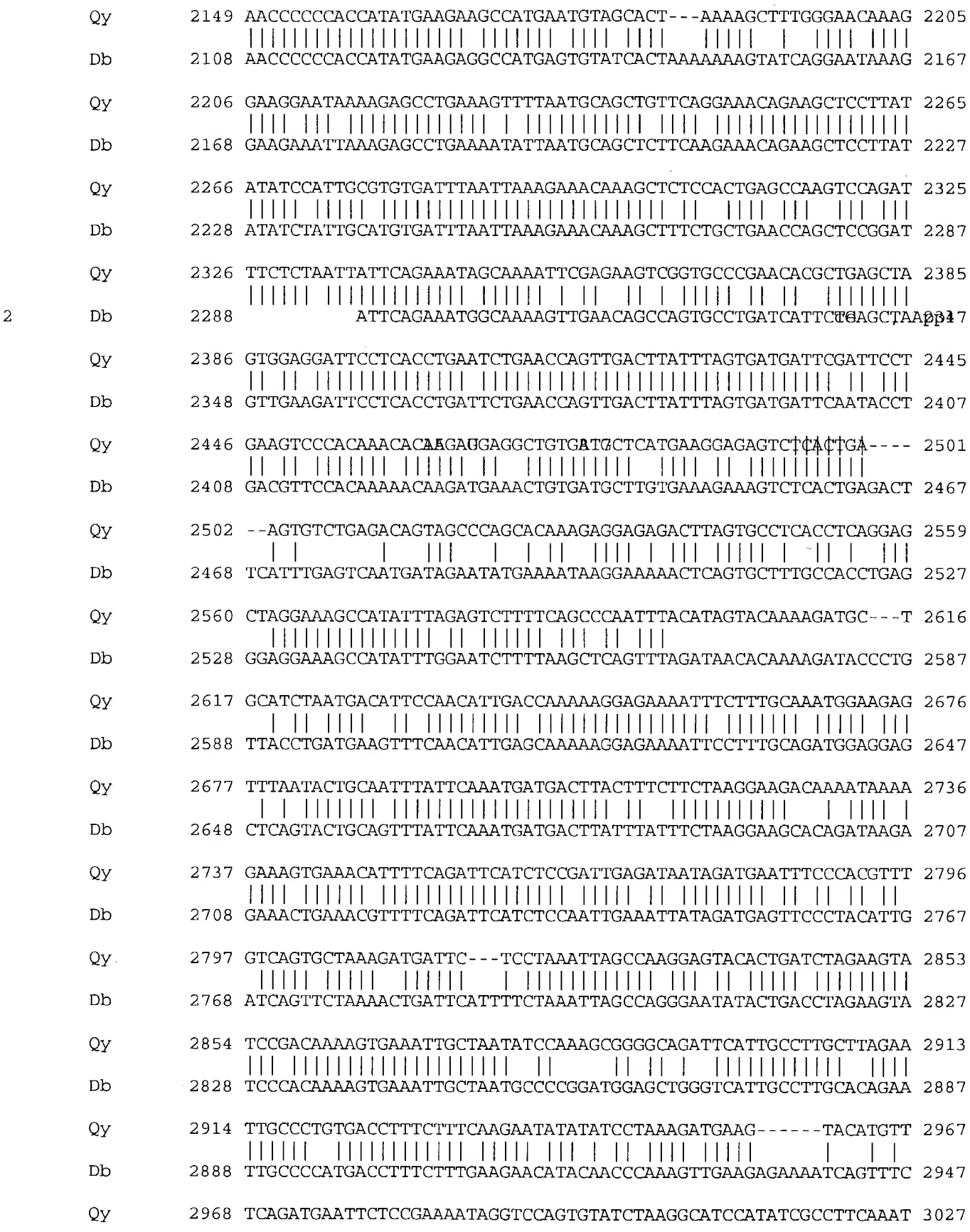
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis -
XX
PS Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
CC ABU11450-ABU11845, described in the disclosure of the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 other;

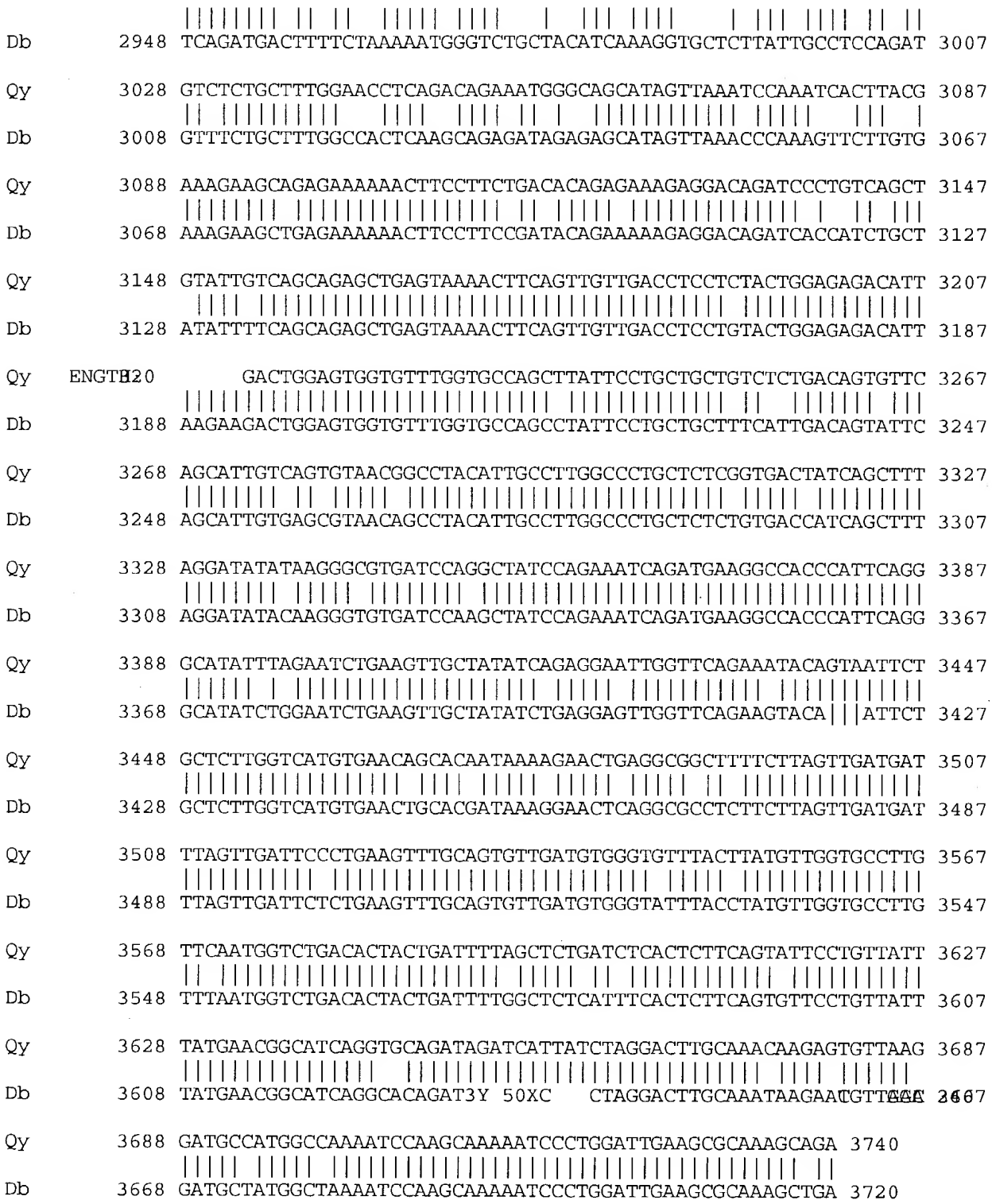
Query Match 61.4%; Score 2297.4; DB 25; Length 4698;
Best Local Similarity 80.7%; Pred. No. 0;
Matches 2996; Conservative 0; Mismatches 596; Indels 121; Gaps 22;

```
Qy        134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
              | || ||| | | |||  ||||||  |||||  | ||||||||||||||||||||||||
Db         23 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGCTC 82

Qy        194 CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA 253
              |||||  |   |    | ||||||||  | ||||||||||||  ||  | ||||  |||||||
Db         83 CTGAGACGCGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCCA 141

Qy        254 TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC 313
              ||||||||  | ||||||||  | |||||  |||||||  ||||||||||  |||||||| |
Db        142 TGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCGC 198

Qy        314 CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG 373
              ||||||  ||||||||||||||||||  ||||||||||||||||||    || || ||||
Db        199 AGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAGG 255

Qy        374 AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC 433
              |||||||  ||||||||  ||  |||||  |||||  |||||  ||||||||||||||||||||
Db        256 AGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGC 315

Qy        434 CCGCAGCCGGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTGC 487
              ||||  ||||||||||||||  ||  | ||||      | ||  |||||||  ||||||  |||
Db        316 CCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTGA 375

Qy        488 TGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCC 547
              ||||||||  | |  ||||  |||||  ||  ||||||||  ||  ||  ||||||||||  |||
```







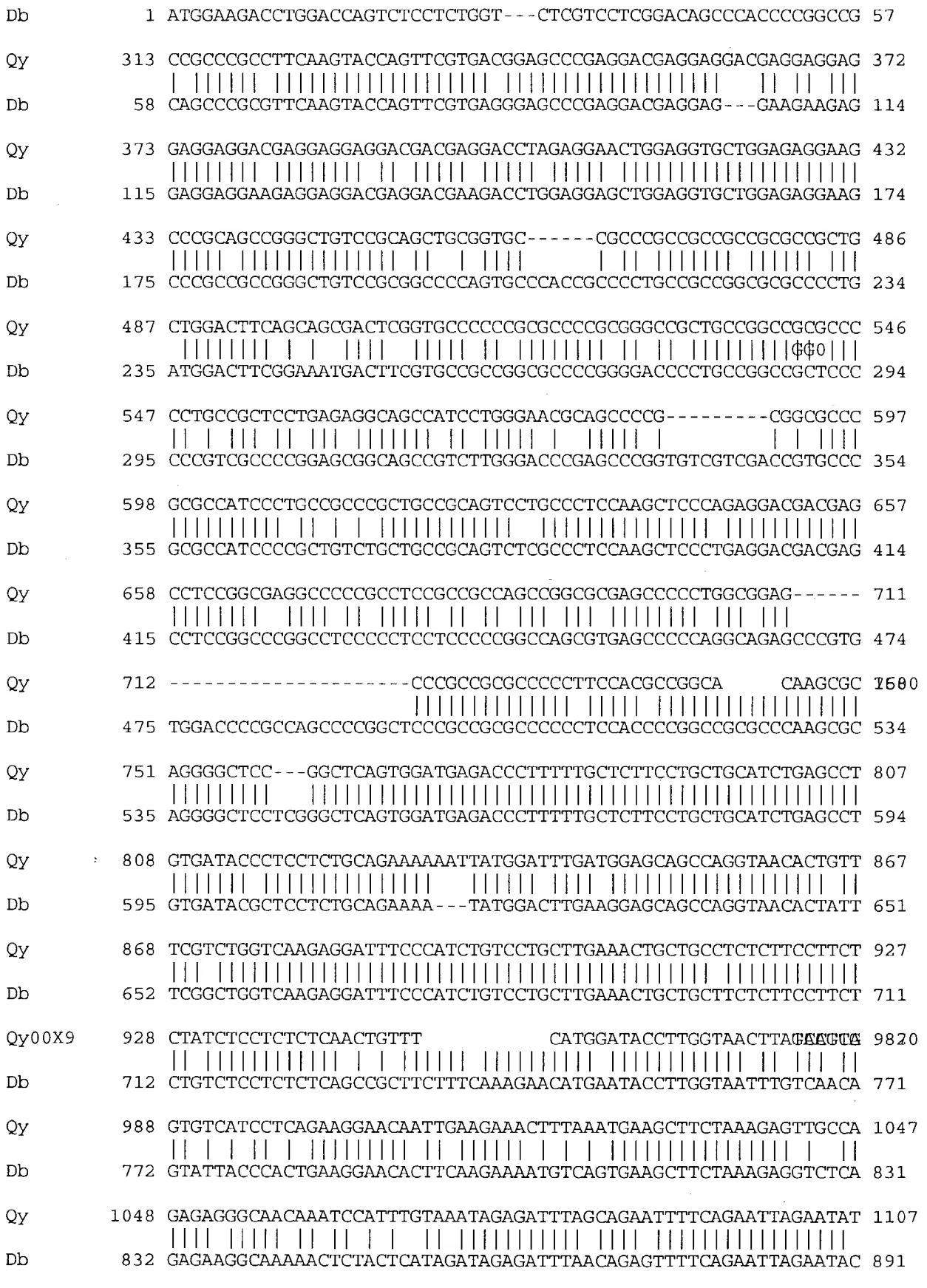


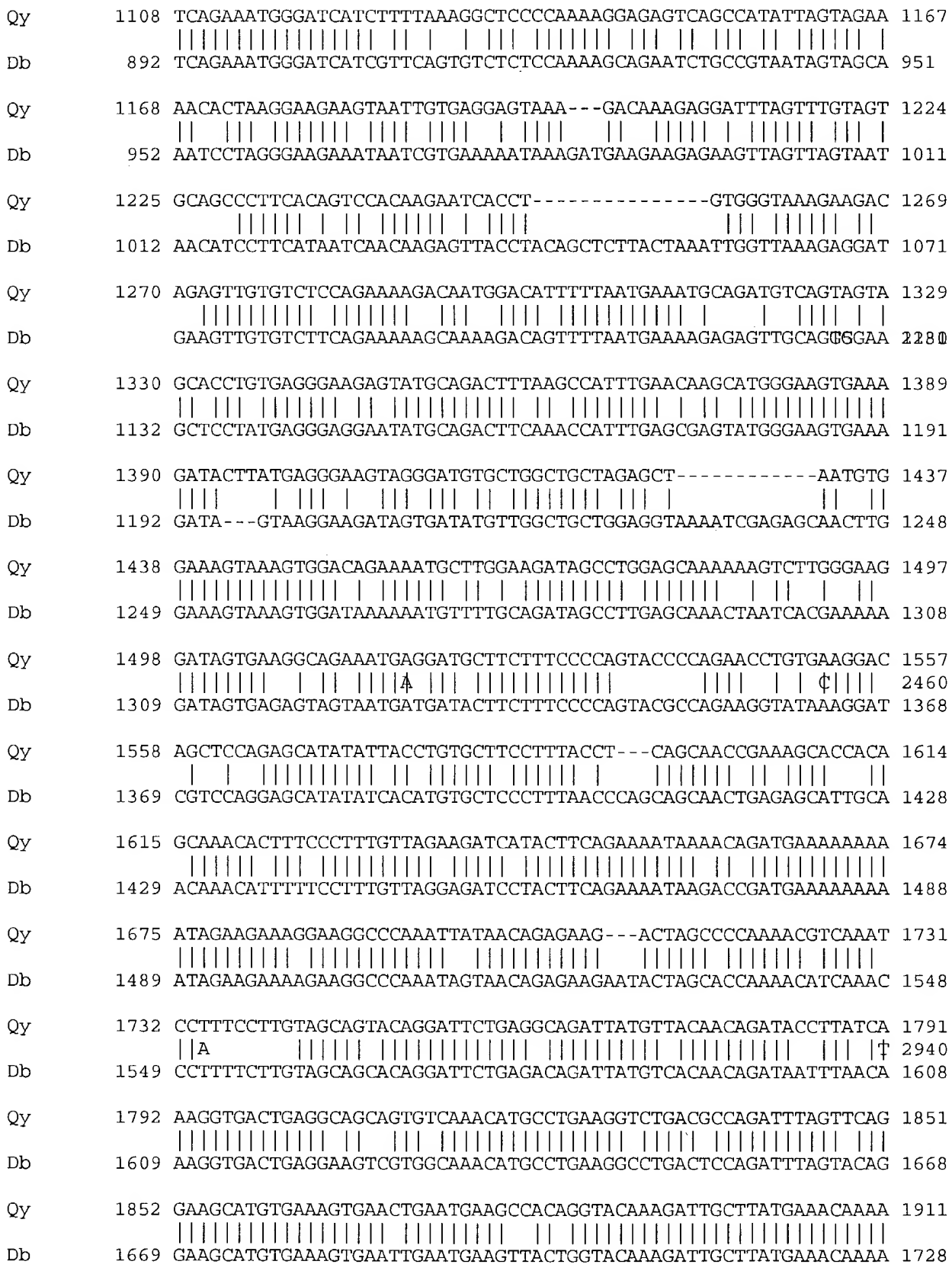
RESULT 8
AAZ56886
ID AAZ56886 standard; DNA; 3579 BP.
XX
AC AAZ56886;

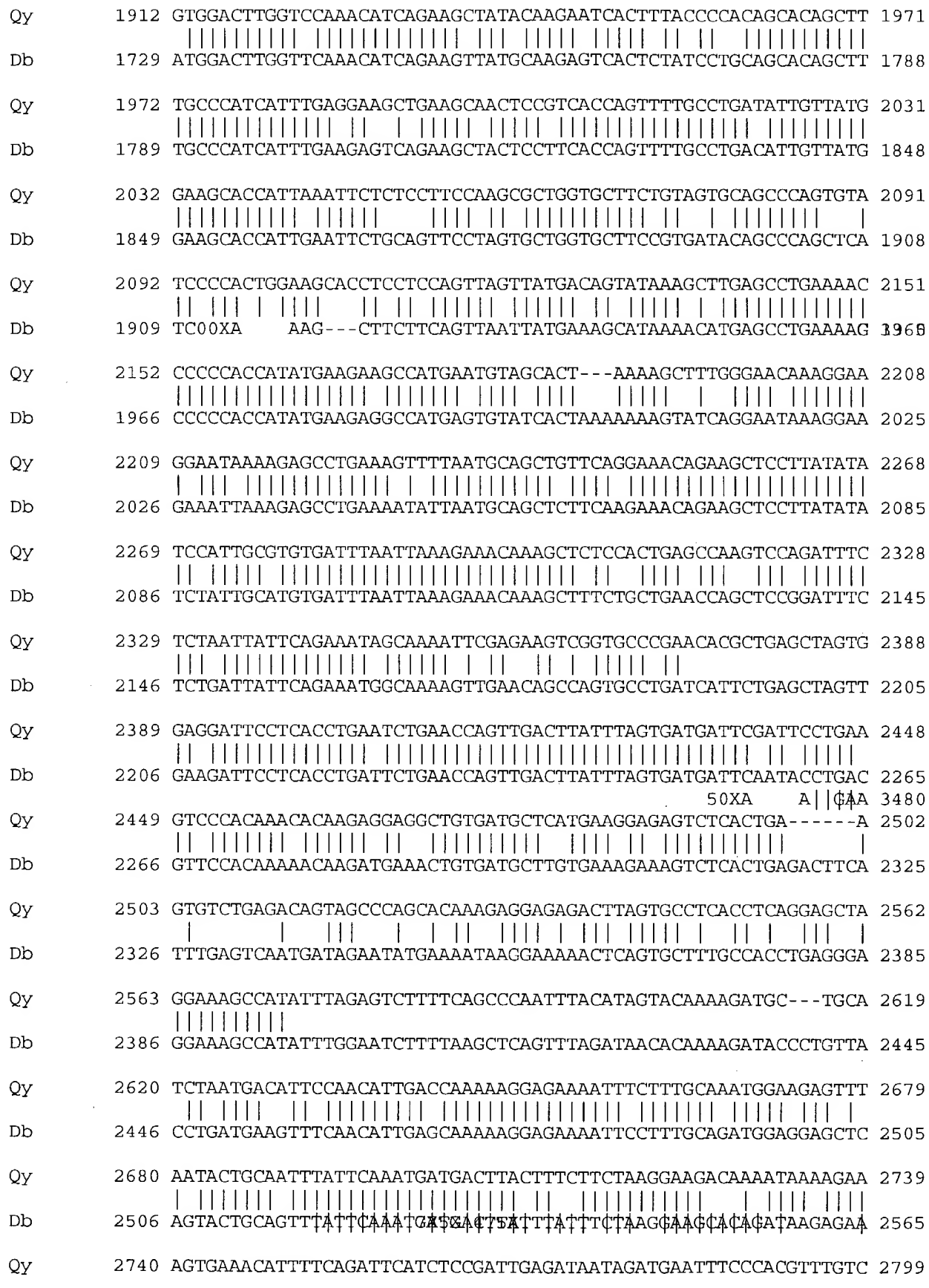
XX
DT 25-APR-2000 (first entry)
XX
DE Human MAGI polypeptide encoding DNA.
XX
KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW psychiatric disorder; developmental disorder; inflammatory disorder;
KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3579
FT /*tag= a
FT /product= "MAGI polypeptide"
XX
PN WO200005364-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-GB02360.
XX
PR 22-JUL-1998; 98GB-0016024.
PR 19-JUL-1999; 99GB-0016898.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha RK;
XX
DR WPI; 2000-182693/16.
DR P-PSDB; AAY569
XX
PT Novel polypeptides related to neuroendocrine-specific proteins and
PT polynucleotides useful for diagnosis of various diseases and for
PT treatment of cancer and neurological disorders -
XX
PS Claim 5; Page 19-20; 35pp; English.
XX
CC The invention relates to human MAGI protein, which is similar to
CC neuroendocrine-specific protein. The MAGI protein can be expressed by
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC and antibodies are useful for treating diseases, including neuropathies,
CC spinal injury, neuronal degeneration, neuromuscular disorders,
CC psychiatric disorders and developmental disorders, cancer, stroke and
CC inflammatory disorders. The polynucleoitde is also useful for chromosome
CC localization and for tissue expression studies. The present sequence
CC represents a DNA encoding the human MAGI protein.
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

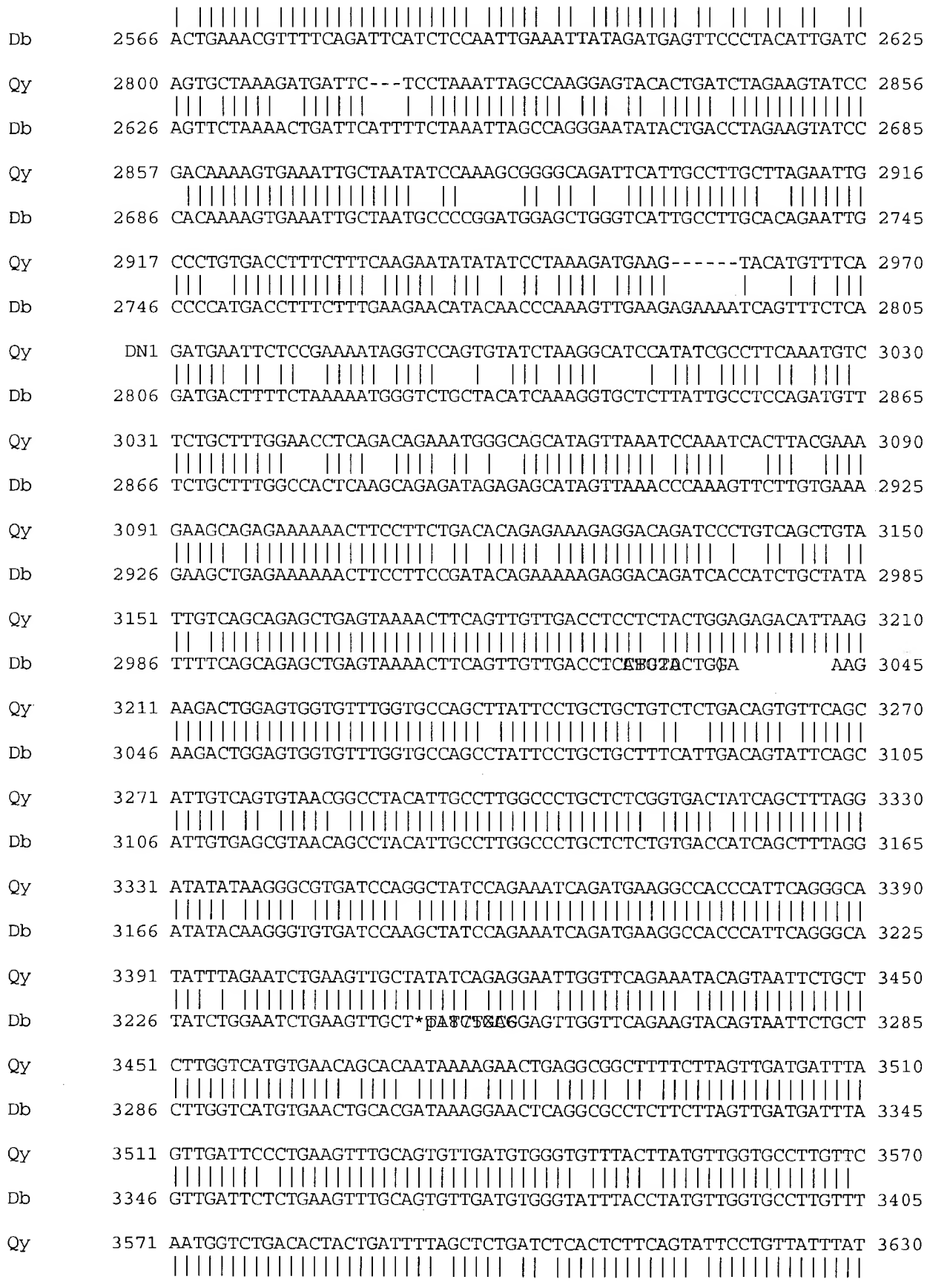
Query Match 61.2%; Score 2289.2; DB 21; Length 3579;
Best Local Similarity 81.5%; Pred. No. 0;
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

Qy 253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
||||||||| | |||||||| | ||||| ||||||| |||||||||| ||||||||









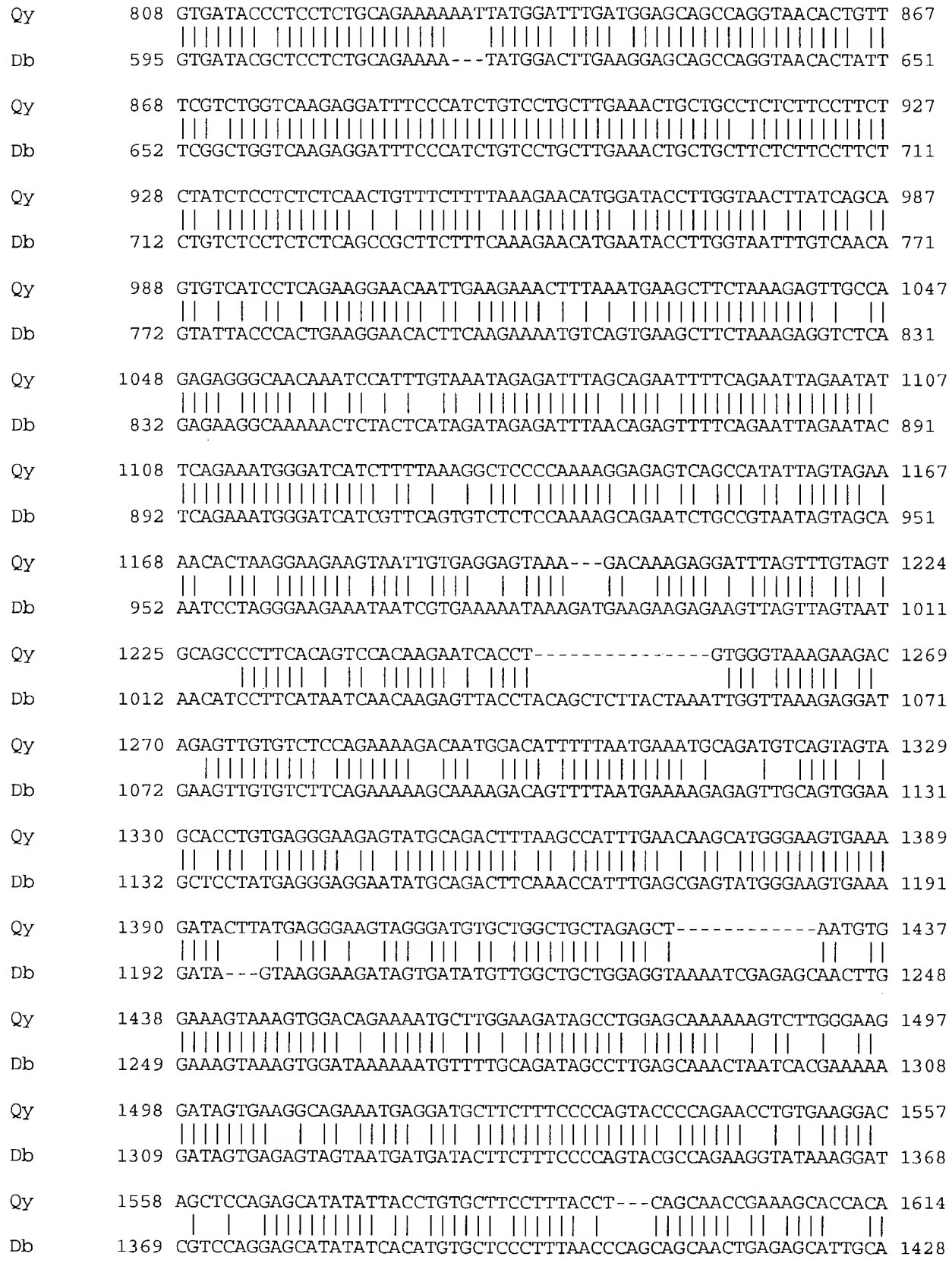
```
Db       3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
              |||||||||||||| |||||||||||||||||||||||||||| |||| |||||| |||
Db       3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
              || ||||| ||||||||||||||||||||||||||||||||||||||| ||
Db       3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575
```

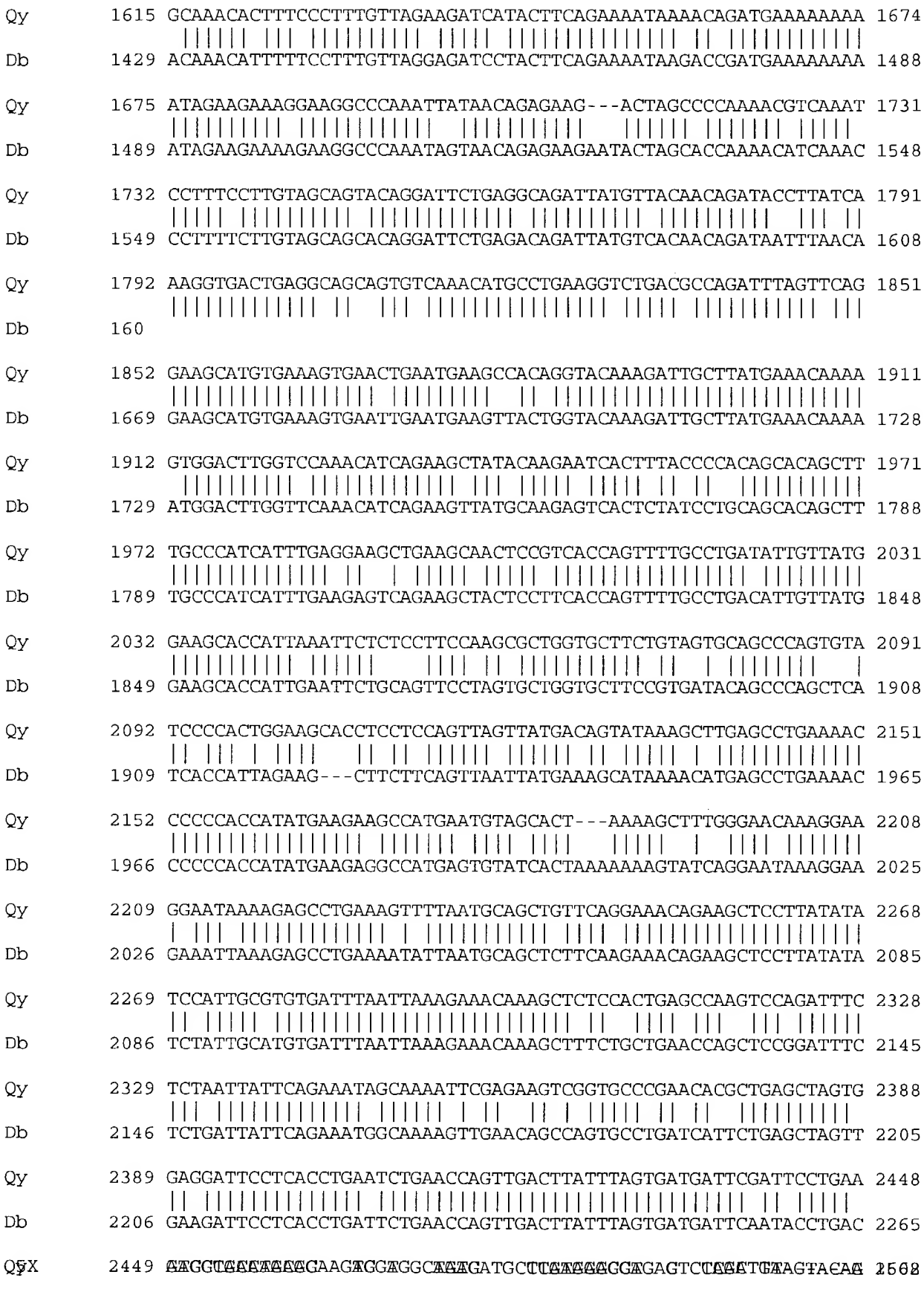
```
RESULT 9
AAF90324
ID   AAF90324 standard; cDNA; 3579 BP.
XX
AC   AAF90324;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Human NOGO-A cDNA.
XX
KW   NOGO-A; human; chromosome 2p21; neuropathy; spinal injury;
KW   brain injury; stroke; neuronal degeneration; Alzheimer's disease;
KW   Parkinson's disease; neuromuscular disorder; psychia ric disorder; T
KW   developmental disorder; neuroprotective; nootropic; neuroleptic;
KW   antiparkinsonian; cerebroprotective; neuroleptic; diagnosis;
KW   therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200136631-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-GB04345.
XX
PR   15-NOV-1999;   99GB-0026995.
PR   24-JAN-2000; 2000GB-0001550.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Michalovich D,  Prinjha R;
XX
DR   WPI; 2001-343822/36.
DR   P-PSDB; AAB82349.
XX
PT   New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT   gene and may be useful in the treatment of neural disorders including
PT   Alzheimer's and Parkinson's diseases  -
XX
PS   Disclosure; Page 25-26; 25pp; English.
XX
CC   The present sequence is that of cDNA encoding human NOGO-A (see
CC   AAB82349).  NOGO-A is a previously known splice variant        G      1167
CC   human NOGO gene on chromosome 2p21.  NOGO-A cDNA was obtained by
CC   PCR amplification of human spinal cord cDNA.  The invention
CC   relates to a novel splice variant, NOGO-C (see AAF90323).  It
```

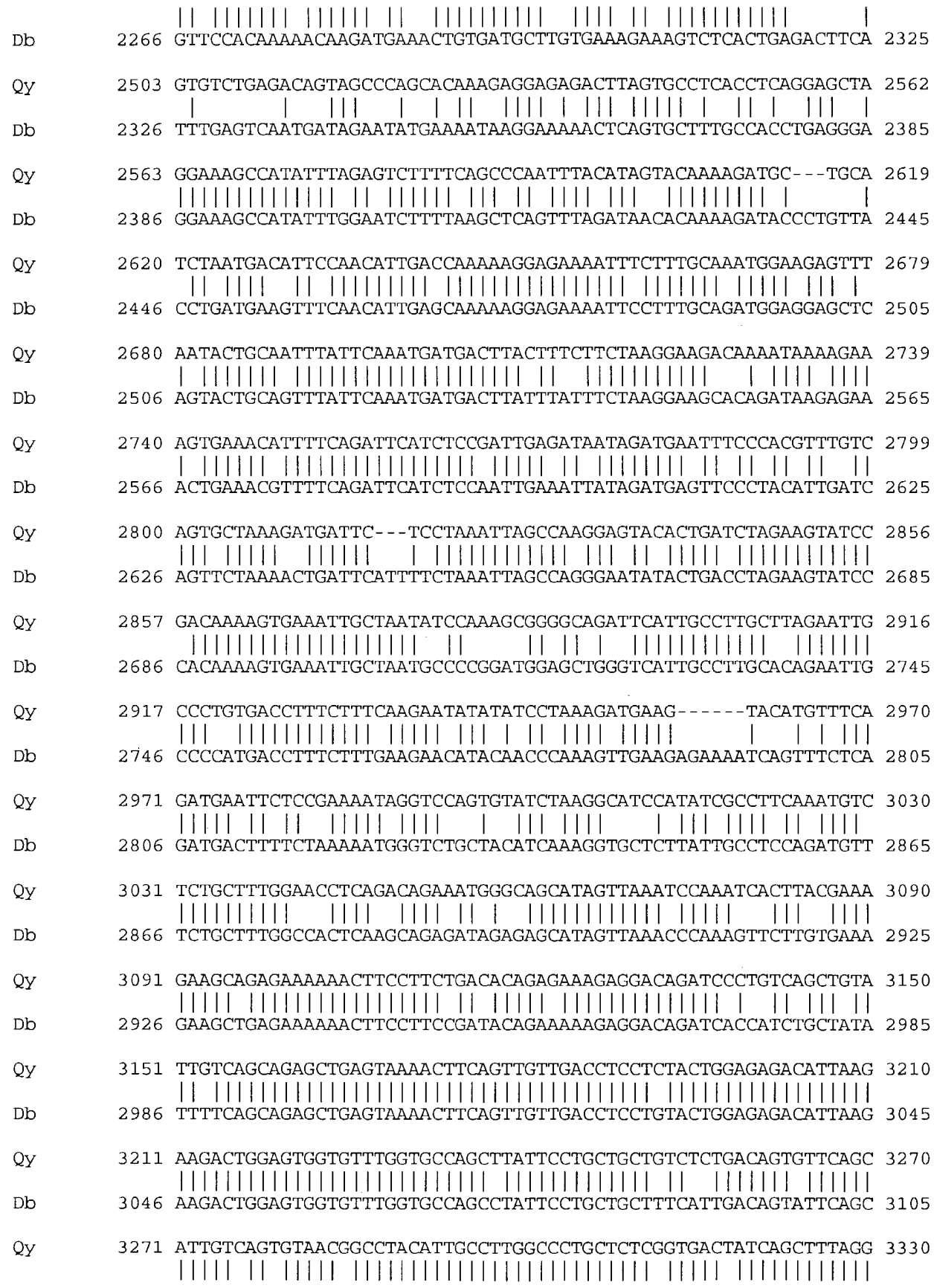
CC provides NOGO-C polypeptides and polynucleotides, and methods for
CC producing such polypeptides by recombinant techniques. Also
CC disclosed are methods for utilising NOGO-C polypeptides and
CC polynucleotides in the treatment of diseases including neuropathies,
CC spinal injury, brain injury, stroke, neuronal degeneration, for
CC example Alzheimer's disease and Parkinson's disease, neuromuscular
CC disorders, psychiatric disorders and developmental disorders. Also
CC provided are methods for identifying agonists and agonists for
CC use in treating conditions associated with NOGO-C imbalance, and
CC diagnostic assays for detecting diseases associated with
CC inappropriate NOGO-C activity or levels.
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 61.2%; Score 2289.2; DB 22; Length 3579;
- Similarity 81.5%; Pred. NACAGA7 -75XT
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

```
Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
              ||||||||| | ||||||||  | |||||  ||||||| |||||||||| ||||||||
Db          1 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 57

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| |||||||||||||||||| ||||||||||||||||||    || || |||
Db         58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||||
Db        115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486

Db        175 CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 234

Qy        487 CTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
              |||||||| | |  |||| ||||| || |||||||| || || |||||||||| |||
Db        235 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy        547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG---------CGGCGCCC 597
              || | ||| || ||| ||||||| || ||||| |  ||||| |         | | ||||
Db        295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 354

Qy        598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
              |||||||||| || | | |||||||||||  |||||||||||||| ||||||||||||
Db        355 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy        658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG------ 711
              ||||||||  |||| || ||||| || || ||| ||| |||||||| ||| |||
Db        415 CCTCCGGCCCCGCCTCCCCTCCTCCCCCGCCAGCGTGAGCCCCAGCCAGAGCCAGAGCTG 474

Qy        712 ----------------------CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
                                   ||||||||||||||| ||||| ||||||||||||||||||
Db        475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGC 534

Qy        751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 594
```





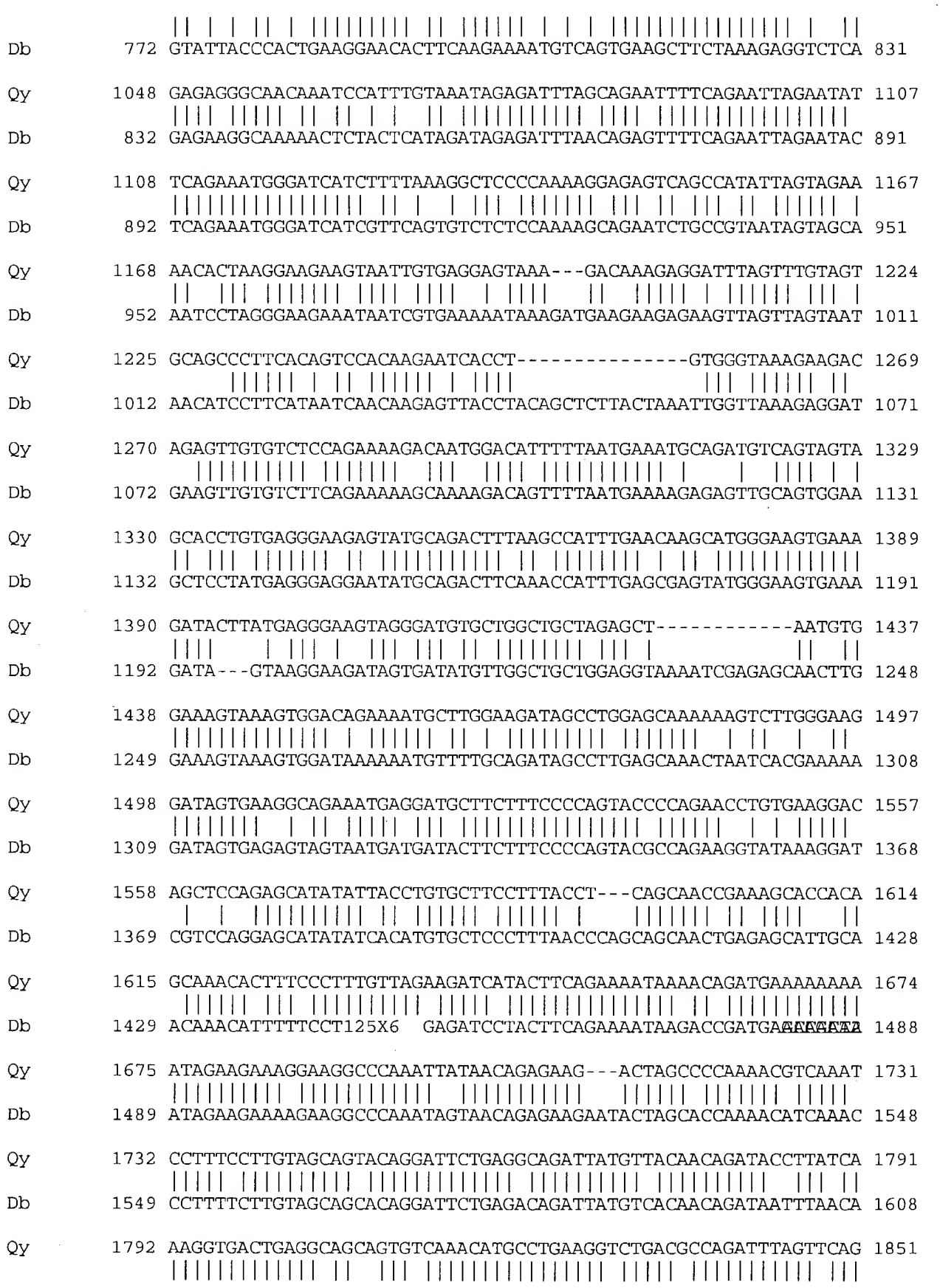


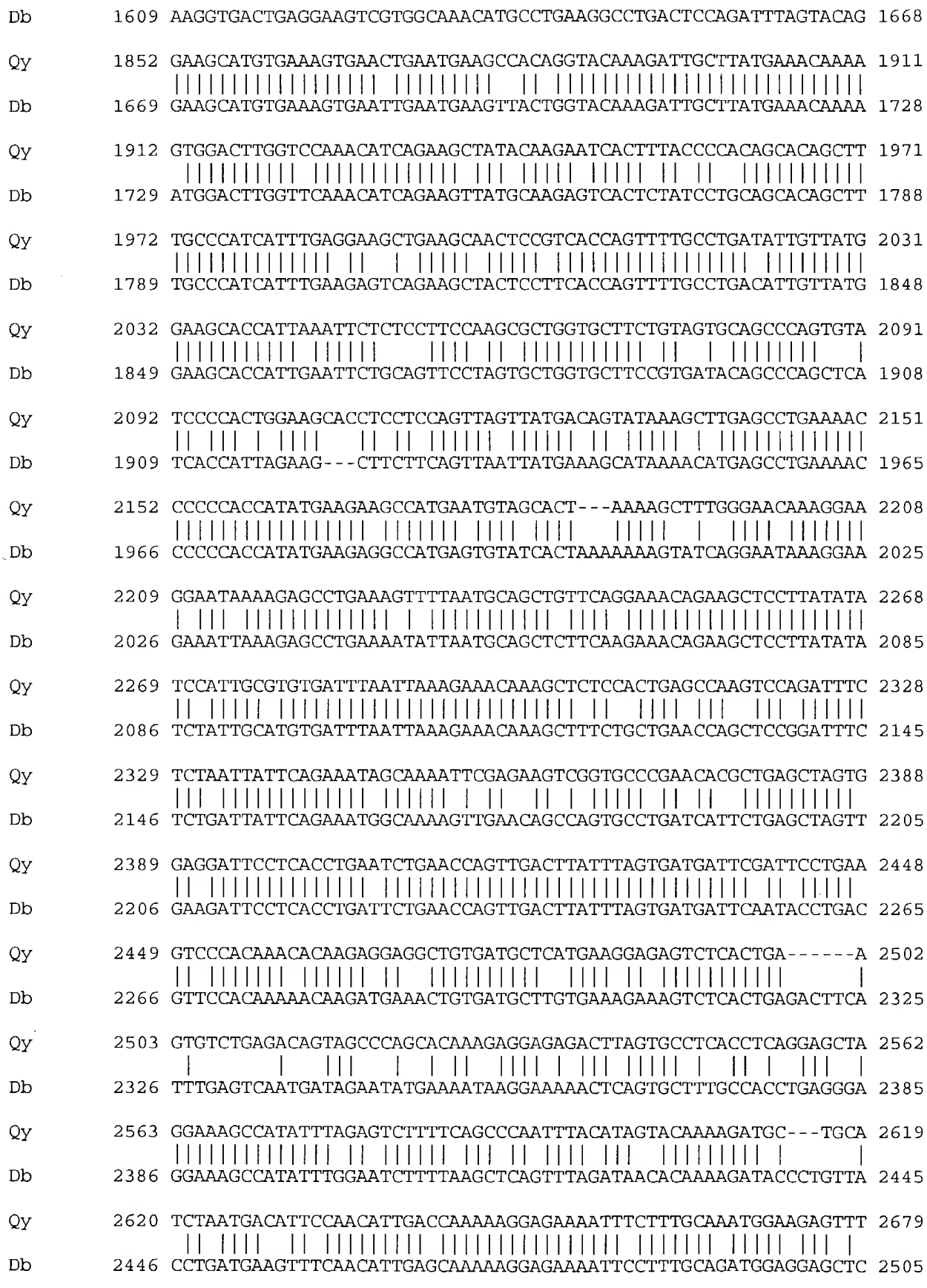
```
Db       3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165

Qy       3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
              ||||| ||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db       3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3225

Qy       3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
              ||| | |||||||||||||||||||| ||||| |||||||||| ||||||||||||||
Db       3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285

Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
              |||||||||||||||| |||| ||||| ||||| ||||| || ||||||||||||||||||
Db       3286 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
              |||||||| |||||||||||||||||||||||| ||||| ||||||||||||||||||
Db       3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
              |||||||||||||||||||||| ||||| || |||||||||| ||||||||||||||
Db       3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
              |||||||||||| |||||||||||||||||||||||||||| |||| |||||| |||
Db       3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
              || ||||| ||||||||||||||||||||||||||||||||||||||||| ||
Db       3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575
```

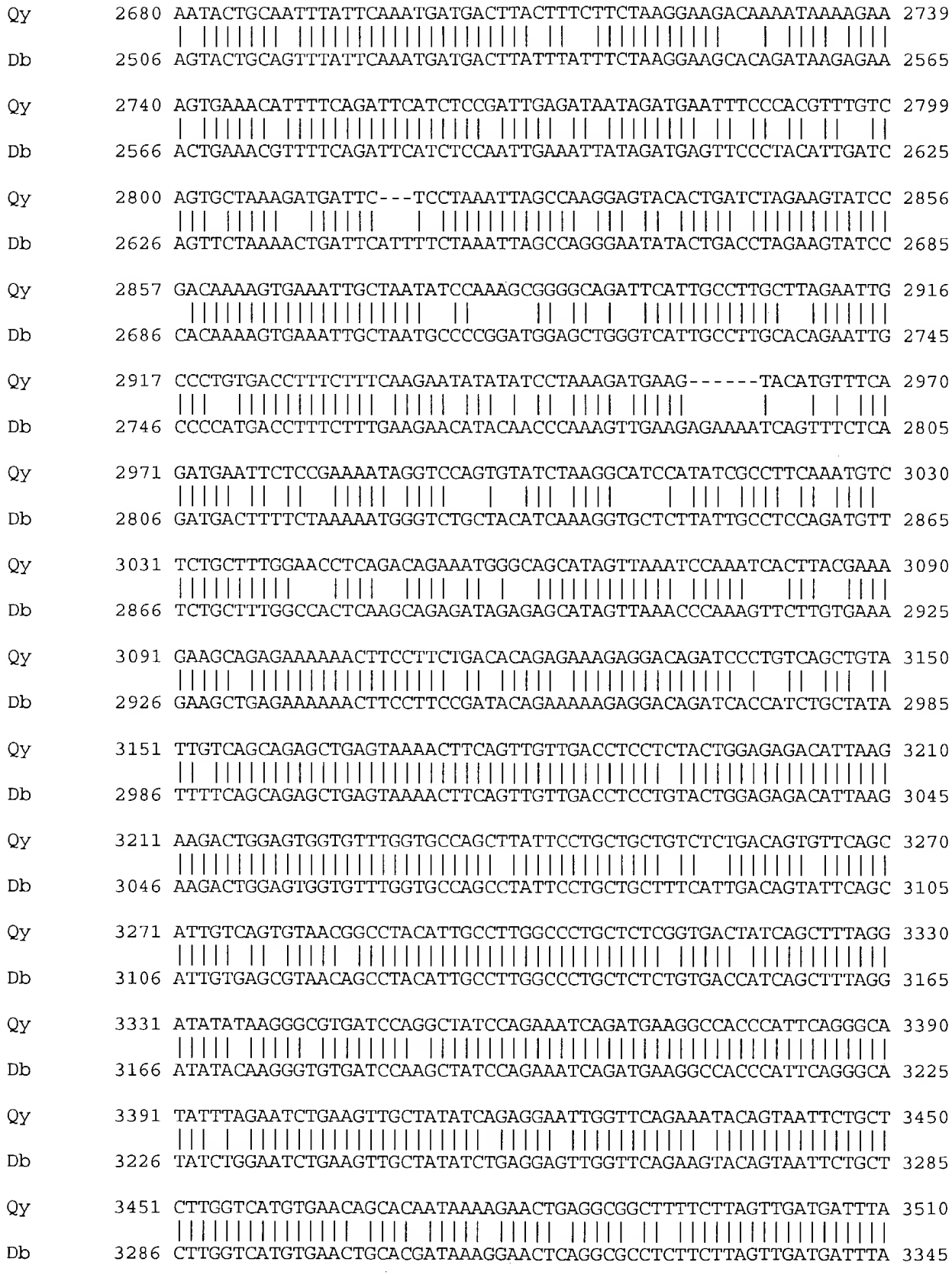
```
RESULT 10
ABN86601
ID   ABN86601 standard; DNA; 3579 BP.
XX
AC   ABN86601;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human neurotransmitter receptor protein Nogo encoding DNA.
XX
KW   Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW   central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW   vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW   nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW   osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW   neurotransmitter receptor; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3579
FT                   /*tag=  a
FT                   /product= "Nogo"
FT                   /note= "Nogo-A, Nogo-B and Nogo-C"
XX
PN   US2002072493-A1.
```

XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-0893348.
XX
PR 19-MAY-1998; 98IL-0124500.
PR 21-JUL-1998; 98WO-US14715.
PR 22-DEC-1998; 98US-0218277.
PR 19-MAY-1999; 99US-0314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR P-PSDB; ABB81078, ABB81079, ABB81080.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in
PT the central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -
XX
PS Disclosure; Page 49-53; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease
CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen.
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

```
  Query Match             61.2%;  Score 2289.2;  DB 24;  Length 3579;
  Best Local Similarity   81.5%;  Pred. No. 0;
  Matches 2925;  Conservative    0;  Mismatches  548;  Indels  117;  Gaps   19;

Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCCGGCCT 312
              ||||||||| | ||||||||  | |||||   ||||||| |||||||||| ||||||||
Db          1 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 57

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| ||||||||||||||||||| ||||||||||||||||||||   || || |||
Db         58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGG GGTGCTGGAGAGGAAG 174

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486
              ||||| |||||||||||||| ||  | ||||      | || ||||||| |||||| |||
Db        175 CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 234

Qy        487 CTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
              |||||||| | |  |||| ||||| || |||||||| || || |||||||||| |||
Db        235 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy        547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG---------CGGCGCCC 597
              || | ||| || ||| ||||||| || ||||| |  ||||| |         | | ||||
Db        295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 354

Qy        598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
              |||||||||| || | | |||||||||||  |||||||||||||| ||||||||||||
Db        355 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy        658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG------ 711
              ||||||||  |||| || ||||| || || ||| ||| |||||||| ||| |||
Db        415 CCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474

Qy        712 ----------------------CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
                                   ||||||||||||||| ||||| |||||||||||||||||
Db        475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGC 534

Qy        751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 594

Qy        808 GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
              ||||||| ||||||||||||||   |||||| |||| |||||||||||||||||| ||
Db        595 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 651

Qy        868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927
              ||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        652 TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT 711

Qy        928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987
              || |||||||||||| | | |||||| |||||||||| |||||||||||  || ||| ||
Db        712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy        988 GTGTCATCCTCAGAAGGAACAATTGAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
```







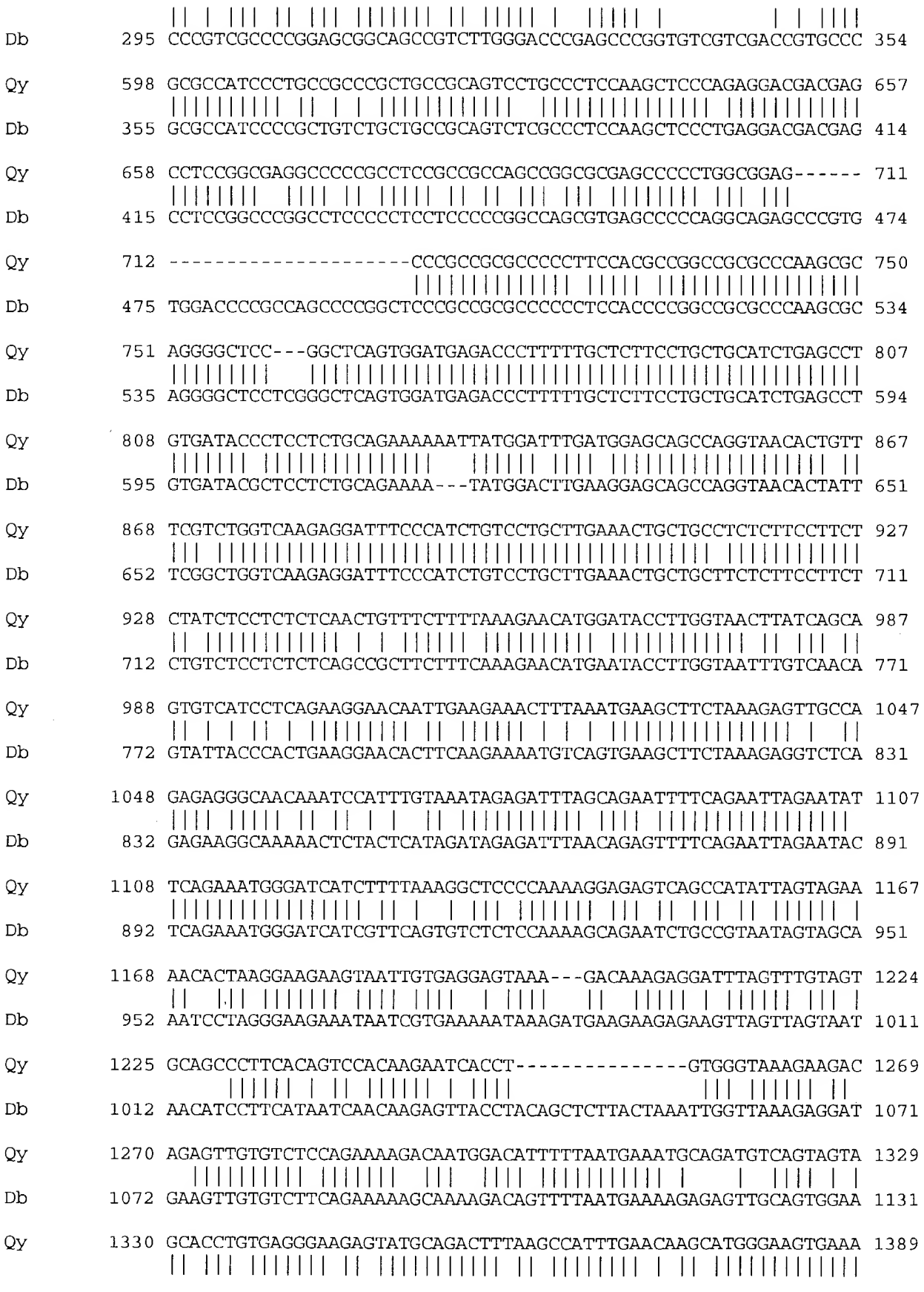
```
Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
             |||||||| |||||||||||||||||||||||| ||||| ||||||||||||||||
Db       3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
             |||||||||||||||||||||| ||||| || |||||||||||| ||||||||||||||
Db       3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
             |||||||||||| |||||||||||||||||||||||||||| |||| |||||| |||
Db       3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
             || ||||| ||||||||||||||||||||||||||||||||||||||||| ||
Db       3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575
```

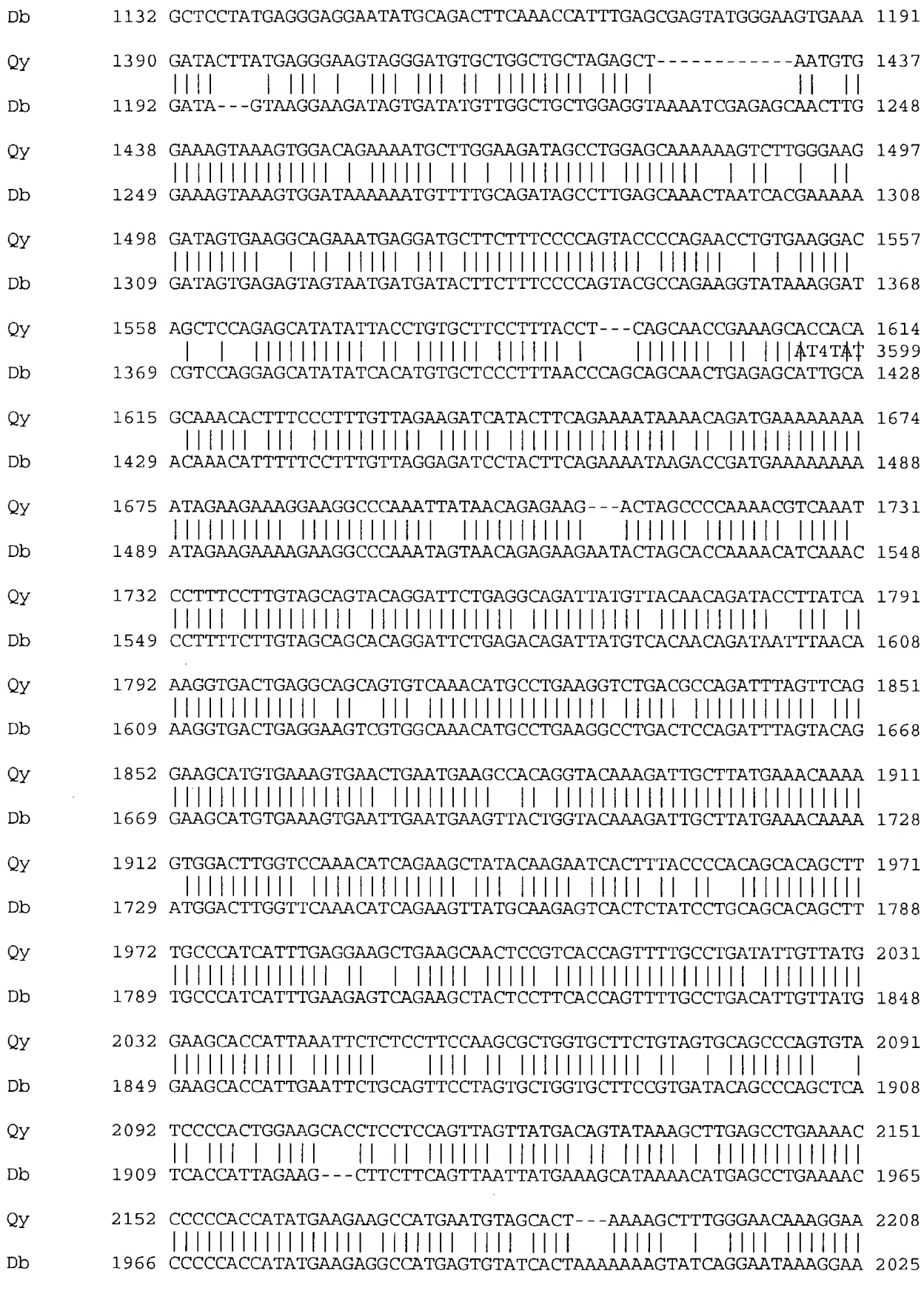
```
RESULT 11
ABK90134
ID   ABK90134 standard; DNA; 3579 BP.
XX
AC   ABK90134;
XX
DT   21-OCT-2002  (first entry)
XX
DE   DNA encoding human NogoA protein.
XX
KW   Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW   stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW   neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW   cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW   tissue hypertrophy; central nervous system; axon regeneration; NogoA;
KW   Nogo-associated disease; metastasis; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3579
FT                   /*tag=  a
FT                   /product= "Human NogoA protein"
XX
PN   WO200257483-A2.
XX
PD   25-JUL-2002.
XX
PF   18-JAN-2002; 2002WO-GB00228.
XX
PR   18-JAN-2001; 2001GB-0001312.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Blackstock WP,  Hale RS,  Prinjha R,  Rowley A;
XX
DR   WPI; 2002-599722/64.
DR   P-PSDB; ABG30938.
XX
```

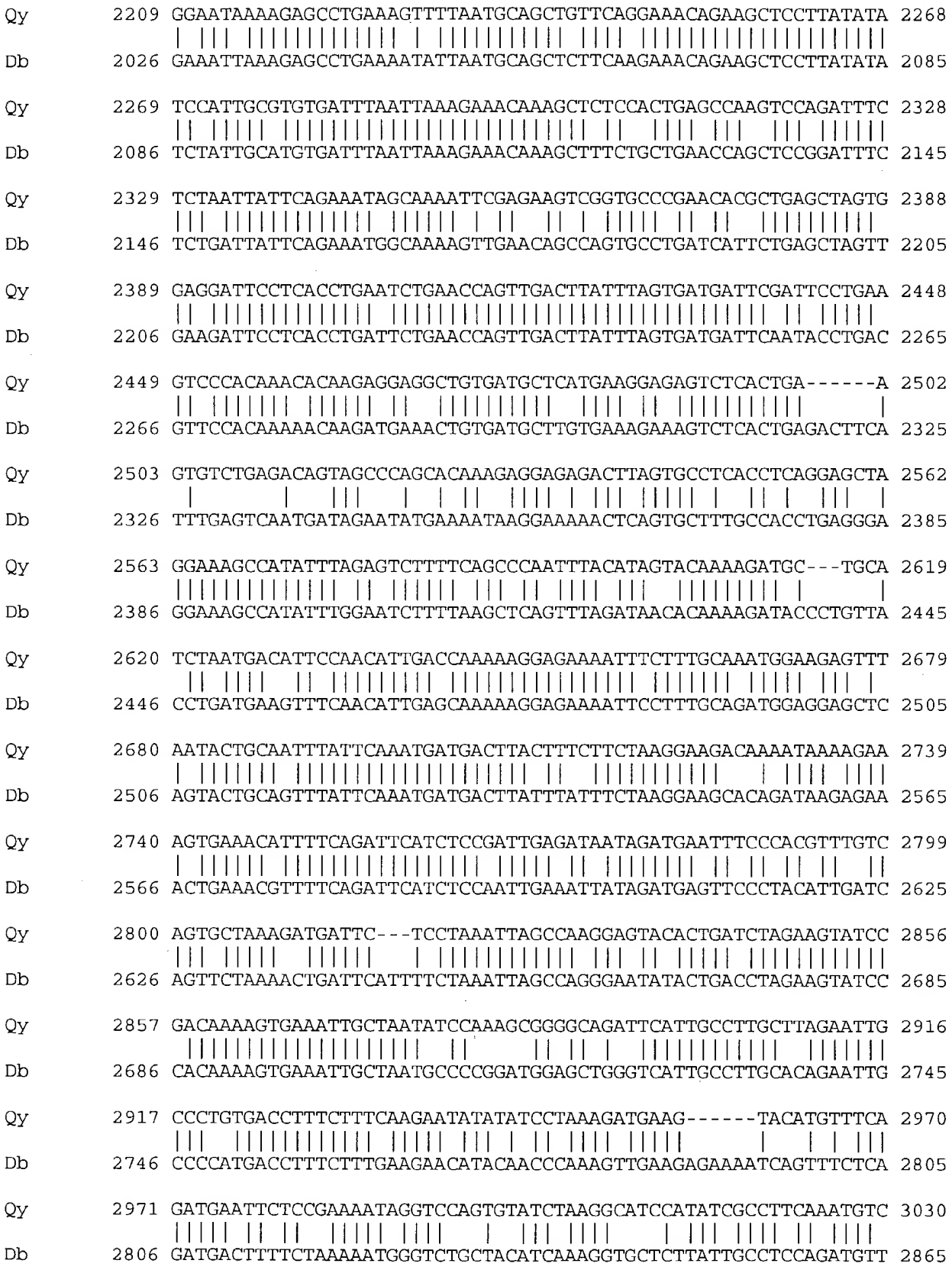
PT Identifying modulators of Nogo or BACE activity for treating acute
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
PT providing and monitoring interaction between Nogo and BACE polypeptides
PT -
XX
PS Disclosure; Page 53-58; 68pp; English.
XX
CC The present invention relates to a new method of identifying modulators
CC of Nogo function or BACE activity. The method involves providing Nogo and
CC BACE polypeptides capable of binding with each other, monitoring the
CC interaction between these polypeptides, and determining if the test agent
CC is a modulator of Nogo or BACE activity. The method is useful in treating
CC acute neuronal injuries, such as spinal or head injury, stroke,
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
CC neuroblastomas), hyperproliferative or dysproliferative disor ers (e.g. 9
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
CC hypertrophy) of the central nervous system. The BACE polypeptide is
CC useful in screening methods to identify agents that may act as modulators
CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in
CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this
CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present nucleic acid sequence encodes the human NogoA
CC protein of the invention.
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 61.2%; Score 2289.2; DB 24; Length 3579;
Best Local Similarity 81.5%; Pred. No. 0;
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

```
Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
              ||||||||| | ||||||||  | |||||   ||||||| |||||||||| ||||||||
Db          1 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 57

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| ||||||||||||||||||| ||||||||||||||||||    || || |||
Db         58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy        433 CCCGCAGCCGGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCCGCCGCTG 486
              ||||| |||||||||||||| ||  | ||||      | || ||||||| |||||| |||
Db        175 CCCGCCGCCGGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 234

Qy        487 CTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
              |||||||| | |  ||||  ||||| || |||||||| || || |||||||||| |||
Db        235 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy        547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG---------CGGCGCCC 597
```




Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191
Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT----------AATGTG 1437
Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248
Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG 1497
Db 1249 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA 1308
Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC 1557
Db 1309 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1368
Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA 1614
Db 1369 CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1428
Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA 1674
Db 1429 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA 1488
Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
Db 1489 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1548
Qy 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791
Db 1549 CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1608
Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851
Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668
Qy 1852 GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911
Db 1669 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728
Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTT 1971
Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788
Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031
Db 1789 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG 1848
Qy 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA 2091
Db 1849 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA 1908
Qy 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151
Db 1909 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC 1965
Qy 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208
Db 1966 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAAGTATCAGGAATAAAGGAA 2025

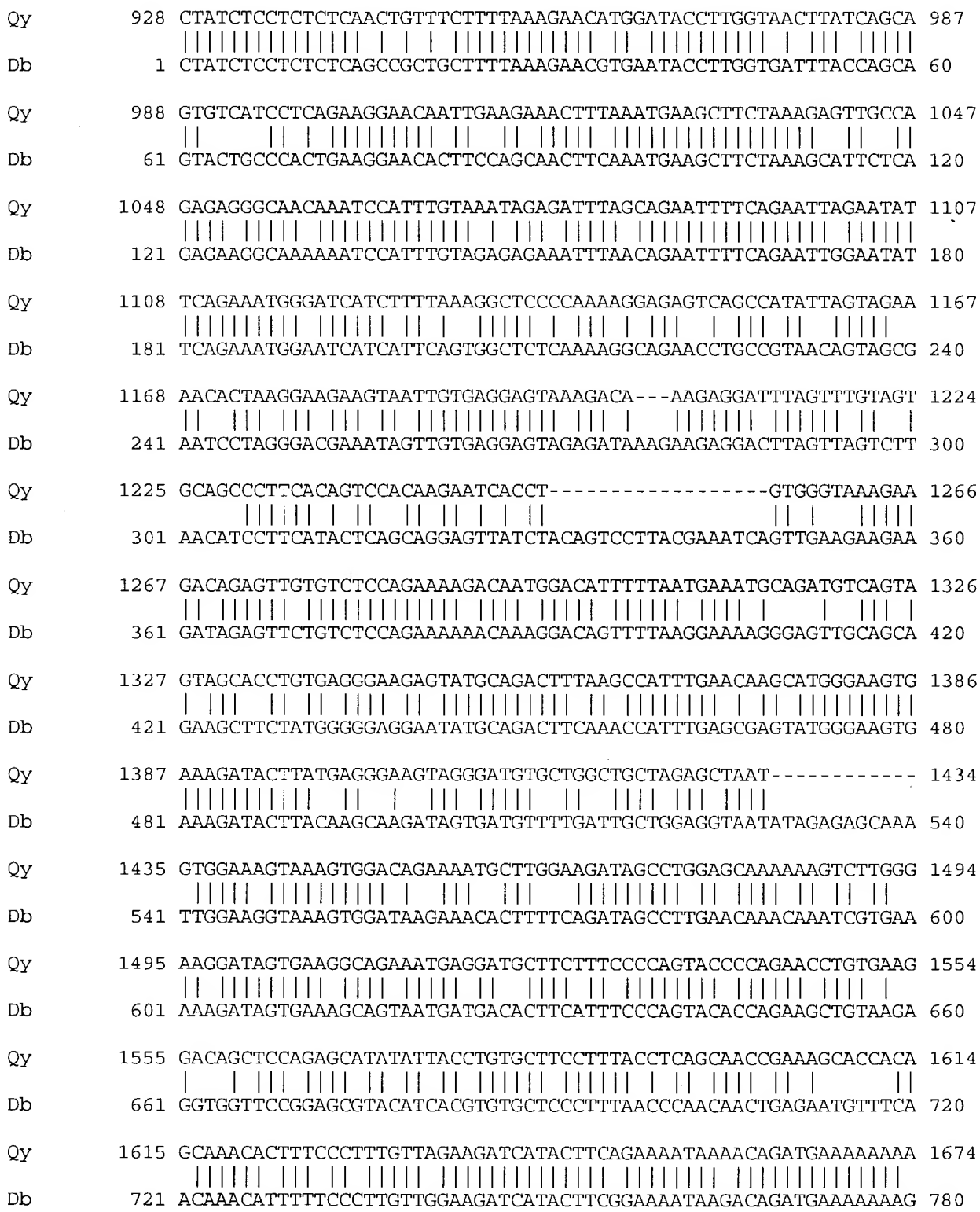


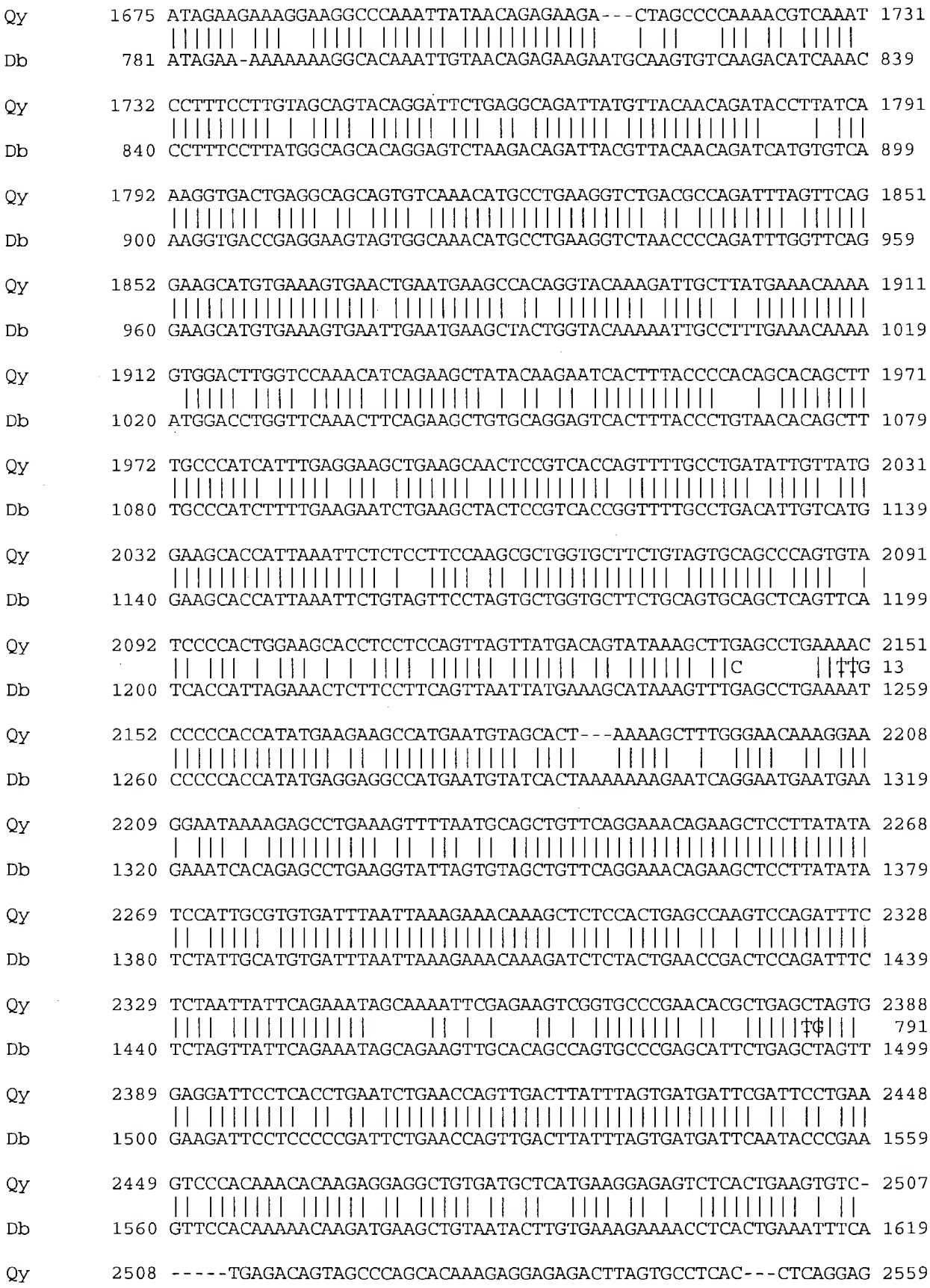
```
Qy       3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
             ||||||||||   ||||  |||| || |  ||||||||||||| |||||   |||  ||||
Db       2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925

Qy       3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150
             |||||  |||||||||||||||||  || |||||  |||||||||||||  |  ||  ||| ||
Db       2926 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 2985

Qy       3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
             || ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       2986 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045

Qy       3211 AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3270
             ||||||||||||||||||||||||||| ||||||||||||  ||  |||||||  ||||||
Db       3046 AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3105

Qy       3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
             |||||  ||  |||||  |||||||||||||||||||||||||  |||||  ||||||||||||
Db       3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165

Qy       3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
             |||||  |||||  ||||||||  ||||||||||||||||||||||||||||||||||||||
Db       3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3225

Qy       3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
             |||  | |||||||||||||||||||  |||||  ||||||||||  ||||||||||||||
Db       3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285

Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
             ||||||||||||||| ||||  |||||  |||||  |||||  ||  ||||||||||||||||
Db       3286 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
             ||||||||  |||||||||||||||||||||||||  |||||  ||||||||||||||||
Db       3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
             ||||||||||||||||||||||  |||||  ||  ||||||||||||  ||||||||||||||
Db       3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
             |||||||||||||  |||||||||||||||||||||||||||||||  ||||  ||||||  |||
Db       3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
             ||  |||||  |||||||||||||||||||||||||||||||||||||||  ||
Db       3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575
```

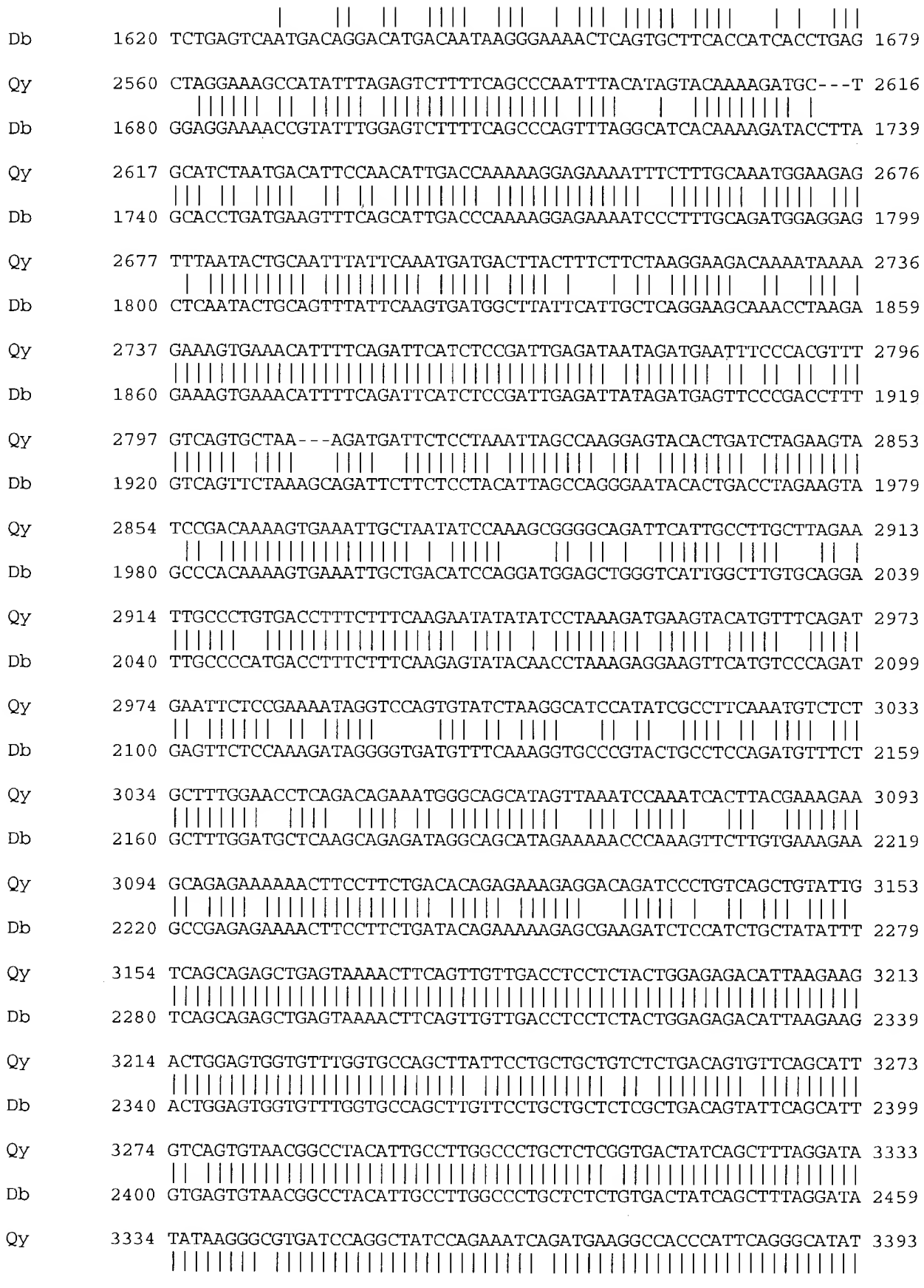
RESULT 12
AAD01174
ID   AAD01174 standard; cDNA; 3833 BP.
XX
AC   AAD01174;
XX
DT   02-NOV-2000 (first entry)
XX

DE Bovine neurite growth inhibitor Nogo cDNA.
XX
KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.
XX
OS Bos sp.
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US26160.
XX
PR 06-NOV-1998; 98US-0107446.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating eoplastic 5
PT disorders of the central nervous system and inducing regeneration of
PT neurons -
XX
PS Claim 26; Fig 12; 122pp; English.
XX
CC The present sequence is a cDNA encoding bovine Nogo protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated. The
CC present sequence was obtained from bovine spinal cord white matter cDNA
CC library. Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promo Nogo activity can be used to treat or prevent hyperprol6fierative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.
XX
SQ Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 other;

Query Match 50.0%; Score 1869.8; DB 21; Length 3833;
Best Local Similarity 80.9%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 492; Indels 55; Gaps 10;







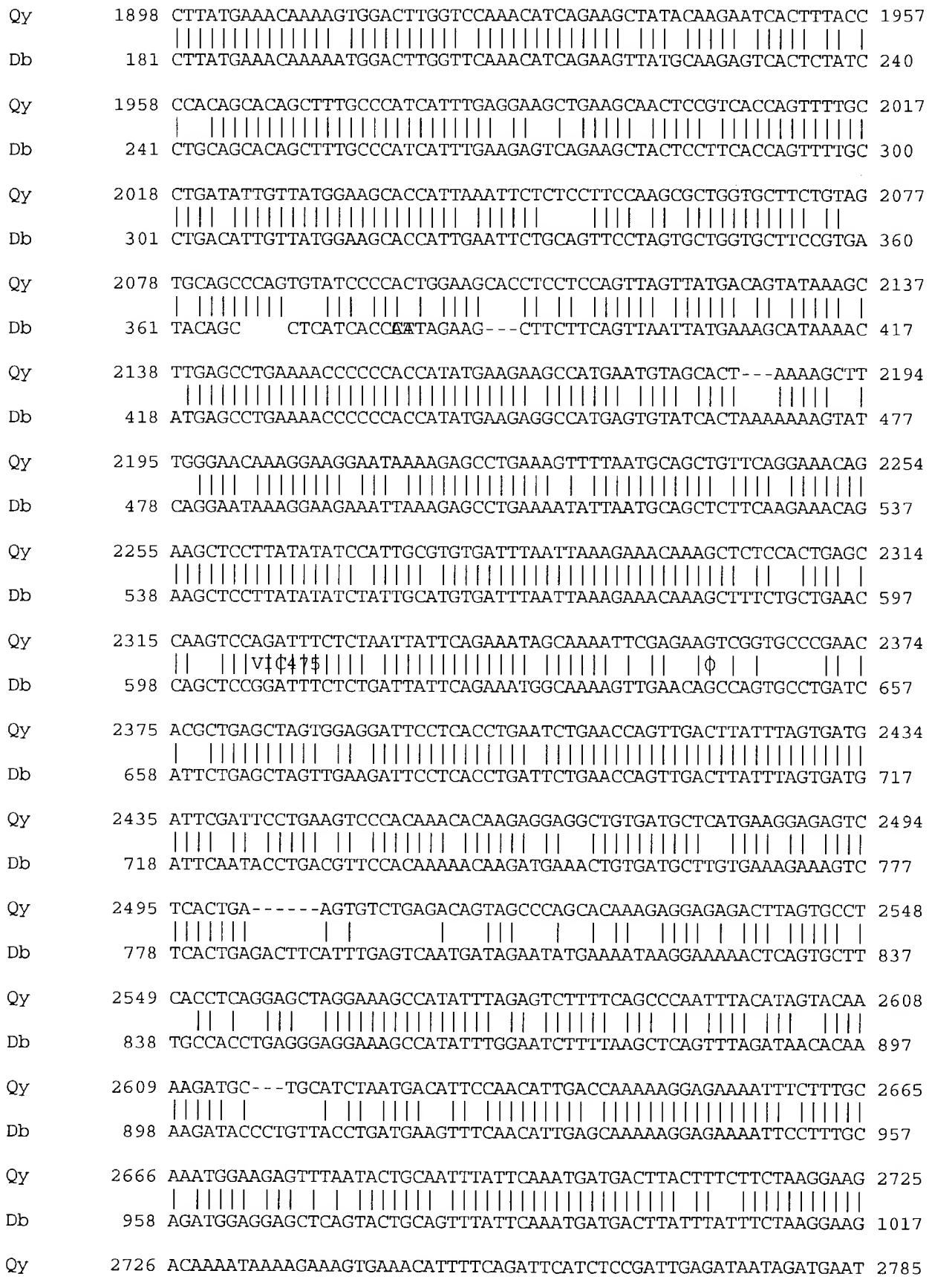
```
Db       2460 TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATAT 2519

Qy       3394 TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTT 3453
              || |||||||||||||||||||| ||||| |||||||||| ||||| ||||||||||||
Db       2520 TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT 2579

Qy       3454 GGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513
              |||||||| ||| |||||||||||||||| || || || ||||||||||||||||||||
Db       2580 GGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT 2639

Qy       3514 GATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT 3573
              ||||| |||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db       2640 GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT 2699

Qy       3574 GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA 3633
              ||||||†¢¢†47$X8||||| |||||||| |||||||||| ||||||||||||||||||
Db       2700 GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA 2759

Qy       3634 CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC 3693
              |||||||||| ||| |||||||||||||| |||||||||| |||| |||||| |||||
Db       2760 CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT 2819

Qy       3694 ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
              ||||| |||||||||||||||||||||||||||||||| ||||| ||
Db       2820 ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA 2866
```

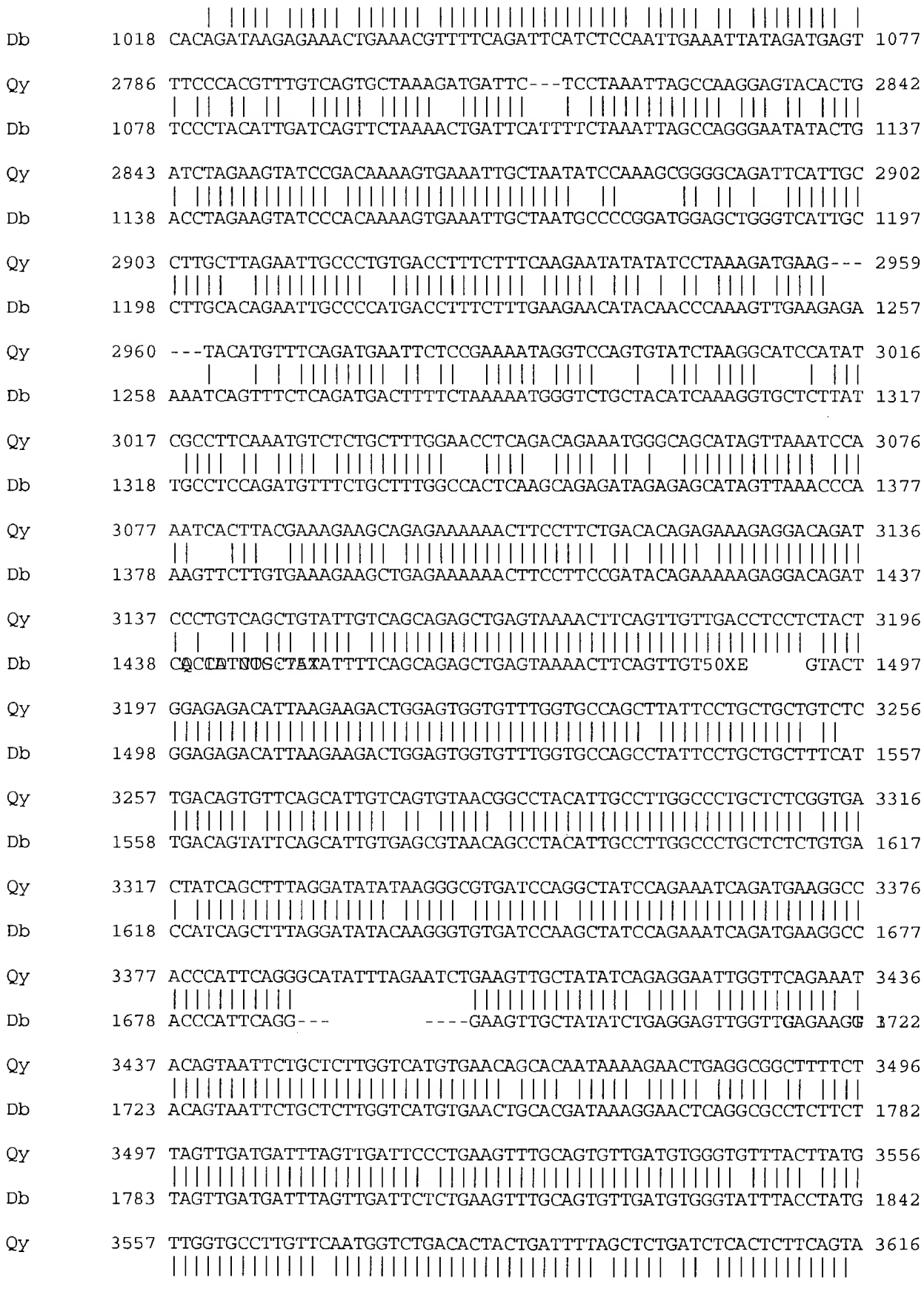
```
RESULT 13
AAV30920
ID   AAV30920 standard; cDNA; 2386 BP.
XX
AC   AAV30920;
XX
DT   14-SEP-1998  (first entry)
XX
DE   Human secreted protein BG160_1 cDNA.
XX
KW   BG160_1; secreted protein; protein factor; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             102..275X|                                    ||
FT                   /*tag=  a
FT   sig_peptide     1863..1899
FT                   /*tag=  b
FT                   /note= "putative leader/signal peptide"
FT   mat_peptide     1900..2027
FT                   /*tag=  c
XX
PN   WO9817687-A2.
XX
PD   30-APR-1998.
XX
PF   24-OCT-1997;   97WO-US19590.
XX
PR   24-OCT-1997;   97US-0740274.
```

PR 25-OCT-1996; 96US-0740274.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1998-261426/23.
DR P-PSDB; AAW58383.
XX
PT Nucleic acid encoding secreted protein from human cells - useful,
PT e.g. as immunomodulator, antitumour agent, promoters of tissue
PT growth, haemostatic and thrombolytic agents etc.
XX
PS Claim 20; Page 74-75; 114pp; English.
XX
CC This cDNA clone, designated BG160_1, codes for a novel human
CC secreted protein (see AAW58383). It was isolated from a human adult
CC brain cDNA library using methods selective for cDNAs that encode
CC secreted proteins. The clone is deposited in composite clone
CC ATCC 98232; an oligonucleotide (see AAT99725) is designed to isolate
CC the clone from the composite. The predicted AT415_4 amino acid
CC sequence shows homology to neuroendocrine-specific proteins. Novel
CC cDNA clones (see AAV30916-32) coding for human secreted proteins (see
CC AAW58580-90) are claimed. These can be used for recombinant
CC production of the secreted proteins for analysis, characterisation,
CC diagnostic or therapeutic use. They can also be used as tissue or
CC mol.wt. markers, for chromosome identification, to identify genetic
CC disorders, to isolate new related DNA, as sources of primers for
CC PCR, to generate antibodies, and in interaction trap assays. The
CC secreted proteins may also have many biological activities, e.g.
CC cytokine, immunomodulator, haematopoiesis regulating activity,
CC tissue growth activity, activin or inhibin activity, chemotactic or
CC chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, antiinflammatory, cadherin and tumour
CC invasion suppressor activity, and tumour inhibition activity. The
CC proteins can be expressed in vivo from DNA, introduced in gene
CC therapy vectors.
XX
SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 other;

Query Match 37.7%; Score 1411.2; DB 19; Length 2386;
Best Local Similarity 83.3%; Pred. No. 1.4e-289;
Matches 1702; Conservative 0; Mismatches 303; Indels 39; Gaps 7;

```
Qy      1718 CCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAA 1777
             ||||||| ||||| ||||| |||||||||| |||||||||||| |||||||||| ||||
Db         1 CCAAAACATCAAACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAA 60

Qy      1778 CAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGC 1837
             ||||||  ||| |||||||||||||| ||  ||| |||||||||||||||| ||||| |
Db        61 CAGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTC 120

Qy      1838 CAGATTTAGTTCAGGAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTG 1897
             |||||||||| |||||||||||||||||||| ||||||||  || ||||||||||||
Db       121 CAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTG 180
```





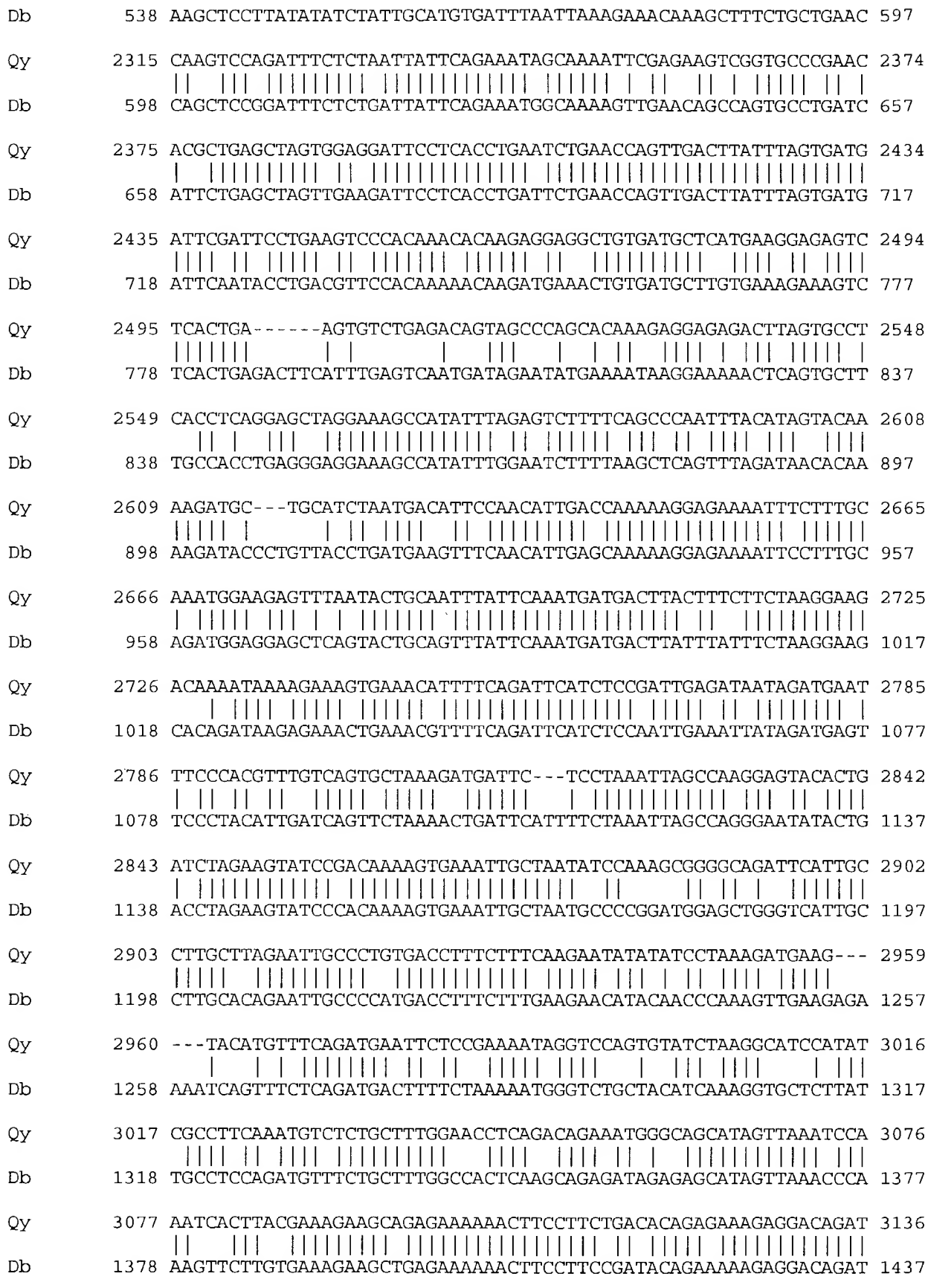
```
Db       1843 TTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 1902

Qy       3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676
              ||||||||||||||||||||||||||  |||||||||||||||||||||||||||||| |
Db       1903 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 1962

Qy       3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736
              ||| |||||| ||||| ||||| ||||||||||||||||||||||||||||||||||||
Db       1963 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 2022

Qy       3737 CAGA 3740
              | ||
Db       2023 CTGA 2026
```

```
RESULT 14
AAF98399
ID   AAF98399 standard; cDNA; 2386 BP.
XX
AC   AAF98399;
XX
DT   07-JUN-2001  (first entry)
XX
DE   Human cDNA clone BG160_1 sequence SEQ ID 41.
XX
KW   Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW   differentiation; immune system modulator; tissue growth; chemotactic;
KW   haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
KW   haematopoiesis.
XX
OS   Homo sapiens.
XX
PN   WO200119988-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US25135.
XX
PR   17-SEP-1999;   99US-0398829.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  McCoy JM,  LaVallie ER,  Collins-Racie LA,  Evans C;
PI   Merberg D,  Treacy M,  Bowman MR,  Spaulding V,  Agostino MJ;
XX
DR   WPI; 2001-244801/25.
DR   P-PSDB; AAB90682.
XX
PT   Isolated nucleic acids encoding polypeptides, useful for modulating
PT   e.g. cytokine and cell proliferation/differentiation activity, the
PT   immune system and hematopoiesis regulating activity -
XX
PS   Claim 1; Page 408-409; 557pp; English.
XX
CC   Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC   proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC   tissue types, and may be used in the prevention, treatment and diagnosis
```

CC of diseases associated with inappropriate protein expression. The
CC polypeptides and nucleic acids may be used as nutrients or to modulate
CC cytokine and cell proliferation/differentiation activity and may also be
CC involved in modulation of the immune system. The cDNA sequences,
CC proteins, their agonists and/or antagonists exhibit haematopoiesis
CC regulating activity; tissue growth activity; activin/inhibin activity;
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; receptor/ligand activity; anti-inflammatory activity;
CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
CC tumour inhibition activity. Included in the invention are probes
CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC encoding the secreted proteins.
XX
SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 other;

Query Match 37.6%; Score 1408; DB 22; Length 2386;
Best Local Similarity 83.2%; Pred. No. 6.5e-289;
Matches 1700; Conservative 0; Mismatches 305; Indels 39; Gaps 7;

```
Qy      1718 CCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAA 1777
             ||||||| ||||| ||||| |||||||||| |||||||||||| |||||||||| ||||
Db         1 CCAAAACATCAAACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAA 60

Qy      1778 CAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGC 1837
             ||||||  ||| |||||||||||||| ||  ||| |||||||||||||| ||||| |
Db        61 CAGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTC 120

Qy      1838 CAGATTTAGTTCAGGAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTG 1897
             |||||||||| |||||||||||||||||||| ||||||||  || ||||||||||||
Db       121 CAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTG 180

Qy      1898 CTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACC 1957
             ||||||||||||| |||||||||| |||||||||||| ||| ||||| ||||| || |
Db       181 CTTATGAAACAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATC 240

Qy      1958 CCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGC 2017
             |  |||||||||||||||||||||||||| ||  | ||||| ||||| ||||||||||||
Db       241 CTGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGC 300

Qy      2018 CTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAG 2077
             |||| |||||||||||||||||| ||||||    |||| || |||||||||| ||
Db       301 CTGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGA 360

Qy      2078 TGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGC 2137
             | ||||||||   ||| ||| | ||||   || || |||||| |||||| || ||||| |
Db       361 TACAGCCCAGCTCATCACCA  AGAAG---CTTCTTCAGTTAATTATGAAAGCAGAAAAC 417

Qy      2138 TTGAGCCTGAAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTT 2194
             |||||||||||||||||||||||||||||| ||||||| |||| ||||   |||||  |
Db       418 ATGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTAT 477

Qy      2195 TGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAG 2254
               |||| |||||||| ||| |||||||||||| | |||||||||| |||| |||||||
Db       478 CAGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAG 537

Qy      2255 AAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGC 2314
             |||||||||||||||| ||||| |||||||||||||||||||||||| ||  |||| |
```



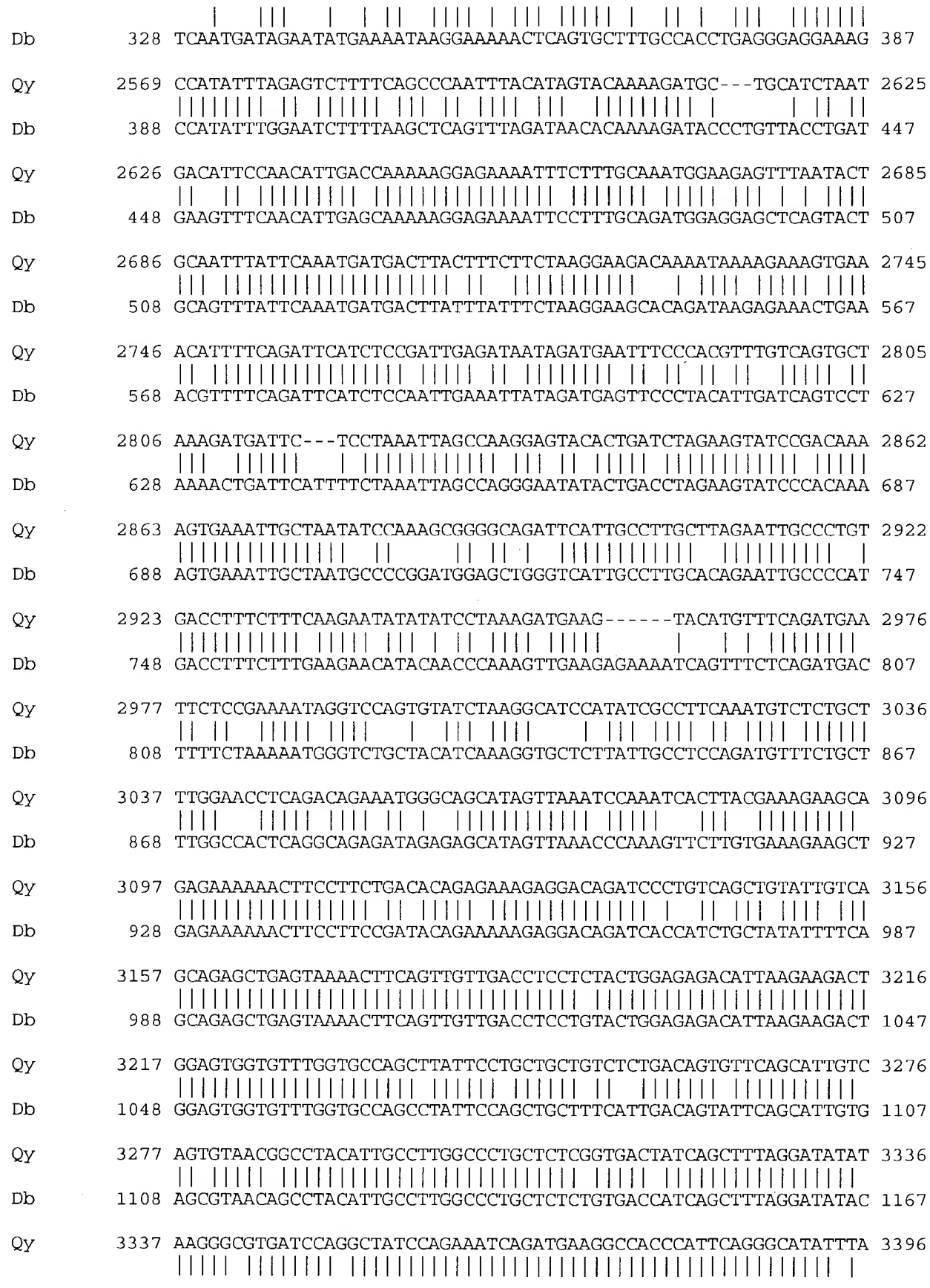
```
Qy       3137 CCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACT 3196
              | |  || ||| |||| ||||||||||||||||||||||||||||||||||||||| ||||
Db       1438 CACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACT 1497

Qy       3197 GGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTC 3256
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||  ||
Db       1498 GGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCAT 1557

Qy       3257 TGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA 3316
              ||||||| |||||||||| || ||||| |||||||||||||||||||||||| ||||
Db       1558 TGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA 1617

Qy       3317 CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC 3376
              | ||||||||||||||||| ||||| |||||||| |||||||||||||||||||||||
Db       1618 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC 1677

Qy       3377 ACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT 3436
              ||||||||||                ||||||||||||| ||||| |||||||||||  |
Db       1678 ACCCATTCAGG---------------GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGT 1722

Qy       3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCT 3496
              |||||||||||||||||||||||||||| |||| ||||| ||||| ||||| || ||||
Db       1723 ACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCT 1782

Qy       3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATG 3556
              |||||||||||||||||||| |||||||||||||||||||||||| ||||| ||||
Db       1783 TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATG 1842

Qy       3557 TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616
              |||||||||||| |||||||||||||||||||||| ||||| |T        G||ATG 1848
Db       1843 TTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 1902

Qy       3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676
              ||  |||||||||||||||||||||  |||||||||||||||||||||||||||||| |
Db       1903 TTGGTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 1962

Qy       3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736
              ||| |||||| ||||| ||||| ||||||||||||||||||||||||||||||||||||
Db       1963 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 2022

Qy       3737 CAGA 3740
              | ||
Db       2023 CTGA 2026
```

RESULT 15
AAI98079
ID   AAI98079 standard; cDNA; 1980 BP.
XX
AC   AAI98079;
XX
DT   04-DEC-2001 (first entry)
XX
DE   Human neuroblastoma expressed polynucleotide SEQ ID NO 22.
XX
KW   Human; neuroblastoma; ss.

XX
OS Homo sapiens.
XX
PN WO200166733-A1.
XX
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-JP01631.
XX
PR 07-MAR-2000; 2000JP-0159195.
PR 12-MAY-2000; 2000JP-0140387.
XX
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
XX
PI Nakagawara A;
XX
DR WPI; 2001-602630/68.
XX
PT Nucleic acids for prognosis of human neuroblastoma comprise nucleic
PT acids expressed by human neuroblastomas -
XX
PS Claim 1; Page 69-70; 159pp; Japanese.
XX
CC The invention relates to nucleic acids (AAI98058-AAI98161) or their
CC homologues expressed by human neuroblastomas useful for detecting genes
CC expressed by neuroblastoma and for analysing their structure and
CC function. The nucleic acids are useful for the diagnosis and prognosis of
CC neuroblastoma.
XX
SQ Sequence 1980 BP; 601 A; 373 C; 423 G; 583 T; 0 other;

Query Match 29.1%; Score 1088.8; DB 22; Length 1980;
Best Local Similarity 83.5%; Pred. No. 3.7e-221;
Matches 1289; Conservative 0; Mismatches 237; Indels 18; Gaps 4;

```
Qy       2215 AAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATT 2274
             ||||||||||||| | |||||||||| |||| |||||||||||||||||||||||| |||
Db         28 AAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT 87

Qy       2275 GCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAAT 2334
             || |||||||||||||||||||||||| ||  |||| |||  ||| |||||||||| ||
Db         88 GCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGAT 147

Qy       2335 TATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGAT 2394
             |||||||||| |||||| | ||  || | ||||| || ||  |||||||||| || |||
Db        148 TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGAT 207

Qy       2395 TCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCA 2454
             |||||||||| |||||||||||||||||||||||||||||| || ||||| || |||
Db        208 TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA 267

Qy       2455 CAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA------AGTGTCT 2508
             |||| |||||  ||  |||||||||  |||| || ||||||||||       | |
Db        268 CAAAAACAAGGTGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAG 327

Qy       2509 GAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAG 2568
```



```
Db       1168 AAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTG 1227

Qy       3397 GAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGT 3456
             |||||||||||||||||||| ||||| |||||||||||| ||||||||||||||||||||
Db       1228 GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGT 1287

Qy       3457 CATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGAT 3516
             ||||||||| |||| ||||| ||||| ||||| || ||||||||||||||||||||||||
Db       1288 CATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT 1347

Qy       3517 TCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGT 3576
             || ||| |||||||||||||||||||| ||||| |||||||||||||||| ||||||
Db       1348 TCTCTGGAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGT 1407

Qy       3577 CTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGG 3636
             |||||||||||||||| ||||| || |||||||||||| ||||||||||||||||||||
Db       1408 CTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGG 1467

Qy       3637 CATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATG 3696
             |||||||  |||||||||||||||||||||||||||| |||| |||||| ||||| |||
Db       1468 CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG 1527

Qy       3697 GCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
             || ||||||||||||||||||||||||||||||||||||||||| ||
Db       1528 GCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 1571
```

Search completed: January 23, 2004, 03:14:18
Job time : 913.477 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:43:47 ; Search time 189.668 Seconds
(without alignments)
8705.823 Million cell updates/sec

Title: US-09-830-972-1
Perfect score: 3741
Sequence: 1 attgctcgtctgggcggcgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2323.8	62.1	4822	4	US-09-484-970B-106	Sequence 106, App
	2	497.4	13.3	799	2	US-08-700-607-2	Sequence 2, Appli
	3	228.8	6.1	1766	4	US-09-149-476-254	Sequence 254, App
	4	228.8	6.1	2664	4	US-09-149-476-255	Sequence 255, App
	5	203.6	5.4	1095	2	US-08-700-607-4	Sequence 4, Appli
	6	180.4	4.8	794	4	US-09-149-476-102	Sequence 102, App
	7	164.6	4.4	261	2	US-08-700-607-9	Sequence 9, Appli
c	8	75.4	2.0	7218	1	US-08-232-463-14	Sequence 14, Appl
	9	75.2	2.0	152331	3	US-09-128-155-16	Sequence 16, Appl
c	10	74.6	2.0	2481	4	US-09-894-998A-35	Sequence 35, Appl
c	11	73.2	2.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli

c	12	73.2	2.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	13	68.6	1.8	319	3	US-09-165-264-8	Sequence 8, Appli
	14	68	1.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	15	68	1.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	16	67.8	1.8	320	3	US-09-165-264-13	Sequence 13, Appl
c	17	67.6	1.8	320	3	US-09-165-264-7	Sequence 7, Appli
	18	67.6	1.8	15378	3	US-08-785-420-1	Sequence 1, Appli
c	19	67.4	1.8	4600	4	US-09-702-705-1797	Sequence 1797, Ap
c	20	67.4	1.8	4600	4	US-09-736-457-1797	Sequence 1797, Ap
c	21	66.8	1.8	320	3	US-09-165-264-11	Sequence 11, Appl
c	22	65.8	1.8	320	3	US-09-165-264-14	Sequence 14, Appl
c	23	64.6	1.7	318	3	US-09-165-264-12	Sequence 12, Appl
c	24	64.6	1.7	8438	1	US-07-945-283-1	Sequence 1, Appli
c	25	63.8	1.7	1926	4	US-09-249-585A-4	Sequence 4, Appli
c	26	63.8	1.7	1931	2	US-09-130-114-2	Sequence 2, Appli
	27	63.6	1.7	4041	3	US-09-105-537-36	Sequence 36, Appl
	28	63.6	1.7	36778	3	US-09-105-537-5	Sequence 5, Appli
	29	63.6	1.7	38506	3	US-09-320-878-19	Sequence 19, Appl
	30	63.6	1.7	38506	4	US-09-141-908-1	Sequence 1, Appli
	31	63.6	1.7	38506	4	US-09-657-440-19	Sequence 19, Appl
	32	61.6	1.6	8438	1	US-07-945-283-1	Sequence 1, Appli
	33	60.8	1.6	2109	4	US-09-370-838-153	Sequence 153, App
c	34	60.6	1.6	1776	1	US-08-722-001-29	Sequence 29, Appl
	35	60.6	1.6	4257	2	US-08-690-473-1	Sequence 1, Appli
	36	60.6	1.6	4257	3	US-09-259-821A-1	Sequence 1, Appli
	37	60.6	1.6	4257	3	US-08-843-659-1	Sequence 1, Appli
c	38	60.6	1.6	12001	1	US-08-458-568A-11	Sequence 11, Appl
	39	60	1.6	2301	1	US-08-306-691B-23	Sequence 23, Appl
	40	60	1.6	2301	4	US-09-167-206-3	Sequence 3, Appli
	41	60	1.6	2301	5	PCT-US93-06251-78	Sequence 78, Appl
c	42	59.4	1.6	426	4	US-09-252-991A-6856	Sequence 6856, Ap
	43	59.4	1.6	552	4	US-09-252-991A-6862	Sequence 6862, Ap
	44	59.4	1.6	570	4	US-09-252-991A-6898	Sequence 6898, Ap
	45	59.4	1.6	723	4	US-09-252-991A-6936	Sequence 6936, Ap

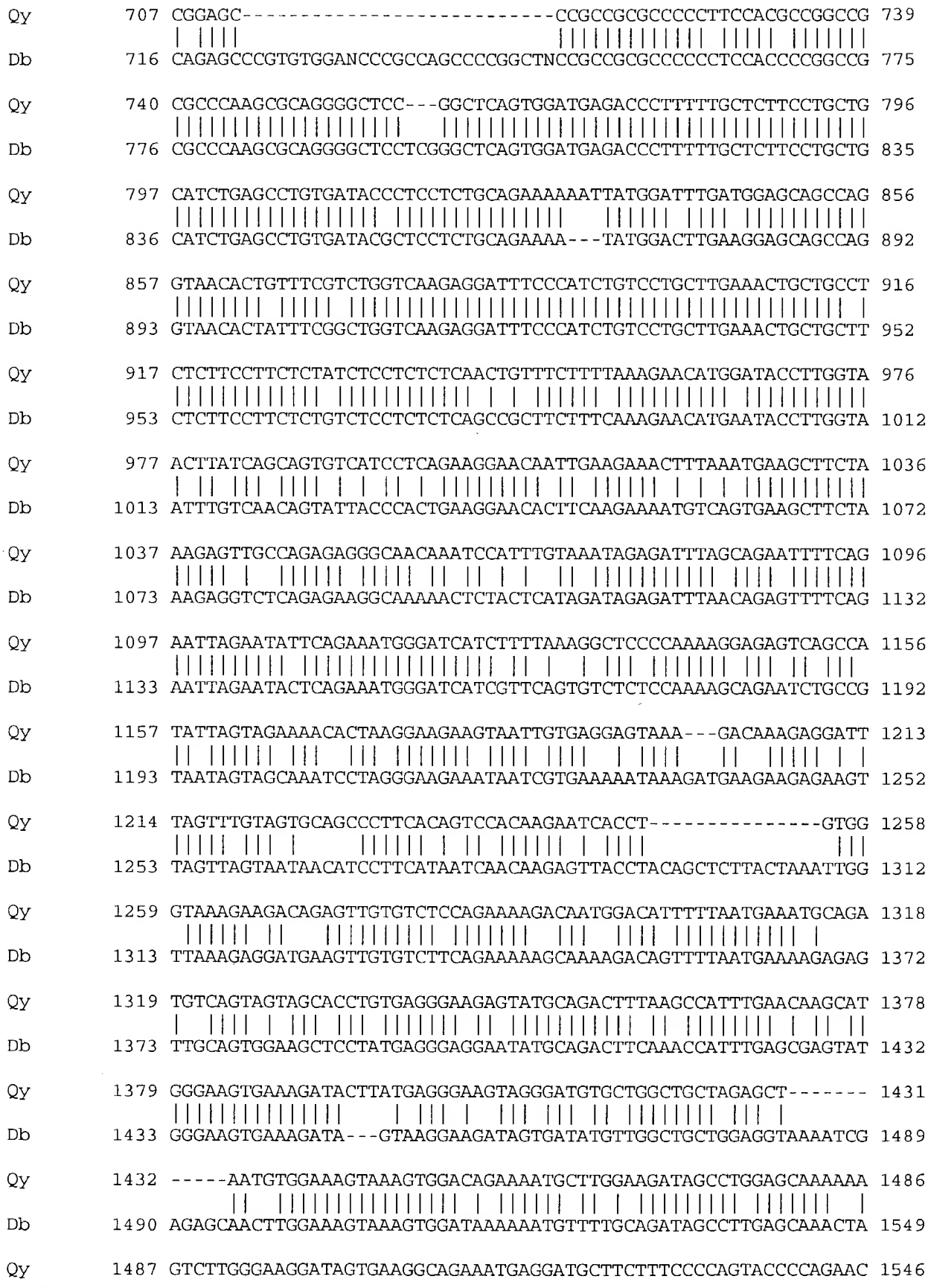
ALIGNMENTS

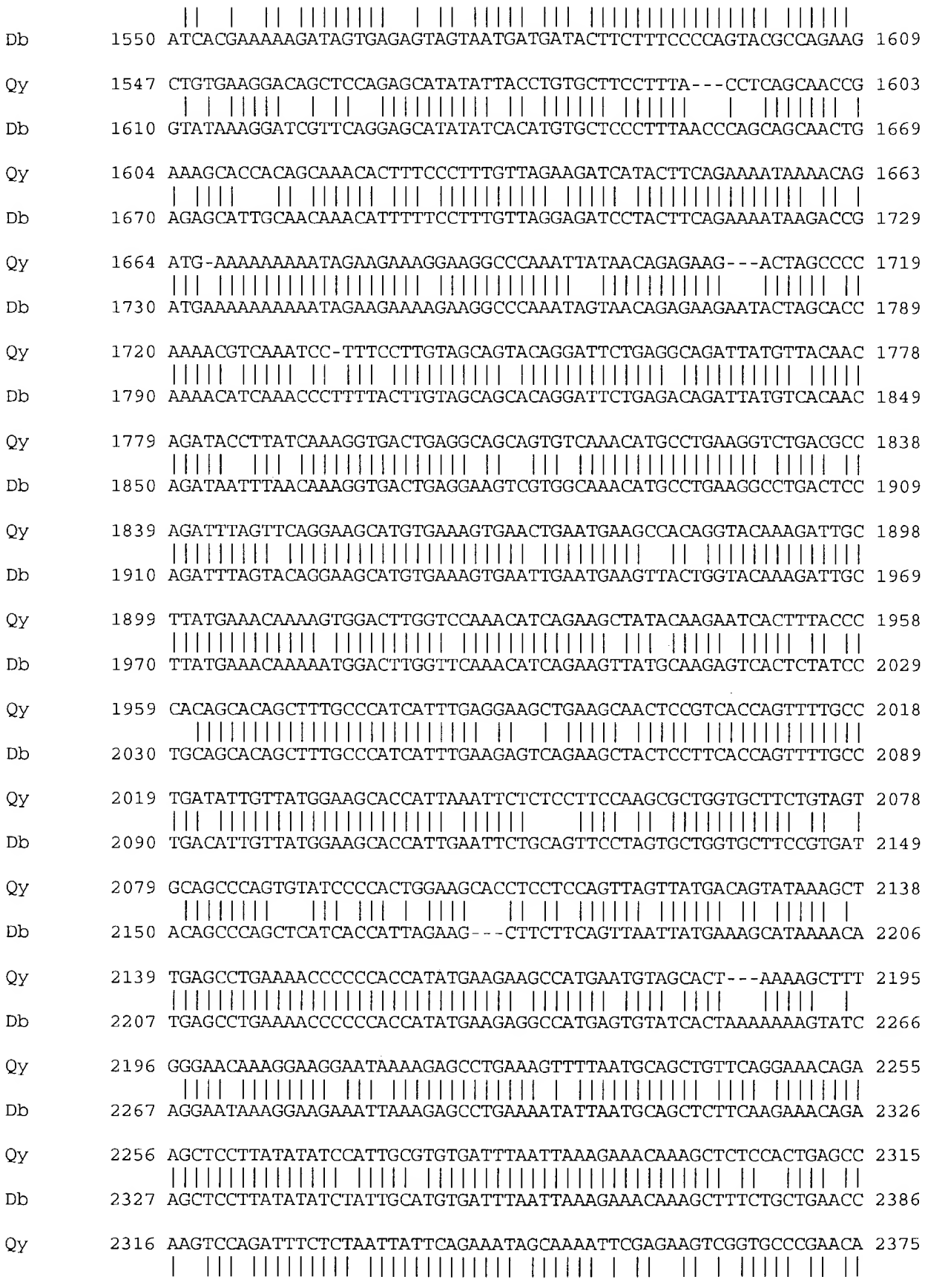
```
RESULT 1
US-09-484-970B-106
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;  APPLICANT:  Jones, Karen A.
;  APPLICANT:  Volkmuth, Wayne
;  APPLICANT:  Walker, Michael G.
;  TITLE OF INVENTION:  BONE REMODELING GENES
;  FILE REFERENCE:  PB-0014 US
;  CURRENT APPLICATION NUMBER: US/09/484,970B
;  CURRENT FILING DATE:  2000-01-18
;  NUMBER OF SEQ ID NOS:  172
;  SOFTWARE:  PERL Program
; SEQ ID NO 106
;   LENGTH: 4822
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

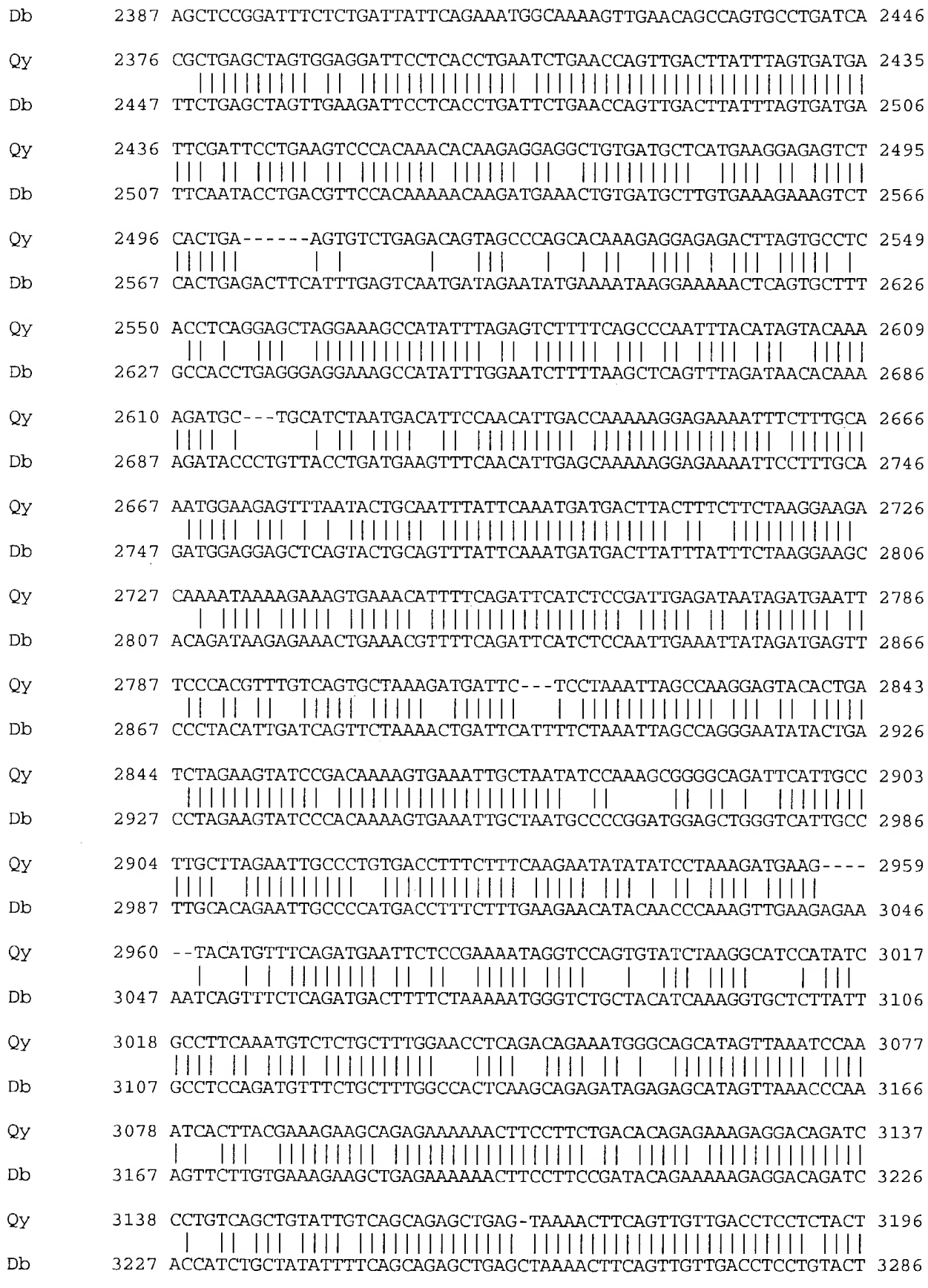
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match 62.1%; Score 2323.8; DB 4; Length 4822;
Best Local Similarity 80.9%; Pred. No. 0;
Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;

```
Qy          63 CGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCG 122
               | || |||||| || |||||||||||||||||||||||||| || | | |||| | |||
Db          78 CNCGGAGGCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCG 137

Qy         123 GCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAAC 182
               |||| |               | |||  ||||||  ||||| | ||||||||||||||
Db         138 GCTCAGT---------------CGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAAC 182

Qy         183 CGCCCCGCGACTCTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCG 241
               |||||||| |||||||  |  ||  |    |||||||| | |||||||||||| ||  |
Db         183 CGCCCGCGGCTCTGAGACGCGGCCCCGGNGGCGGCGGCAGCAGCTGCAGCATCATC-TCC 241

Qy         242 ACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCC 301
               |||| |||||||||||||| | ||||||||  | |||||   ||||||| |||||||||
Db         242 ACCCTCCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCC 298

Qy         302 CGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGG 361
               | |||||||| | |||||| |||||||||||||||||| ||||||||||||||||||||
Db         299 CACCCCGGCCGCAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG- 357

Qy         362 ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC 421
                 || || ||||| || || |||||||| || ||||| ||||| ||||| ||||||||||
Db         358 --GAAGAAGAGGANGATGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGC 415

Qy         422 TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCG 475
               |||||||||||||||| |||||||||||||| ||  | ||||      | || |||||||
Db         416 TGGAGAGGAAGCCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCG 475

Qy         476 CCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGC 535
                ||||||  |  |||||||| | |  ||||  ||||| || |||||||| || || ||||
Db         476 GCGCGCCNNTAATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGC 535

Qy         536 CGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG------ 589
               ||||||| ||||| | ||| || ||| ||||||| || ||||| |  ||||| |
Db         536 CGGCCGCTCCCCCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGT 595

Qy         590 ---CGGCGCCCGCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAG 646
                  | | |||||||||||||| || | | |||||||||||  |||||||||||||| |
Db         596 CGACCGTGCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTG 655

Qy         647 AGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGG 706
               ||||||||||||||||||  |||| || ||||| || || ||| ||| |||||||| ||
Db         656 AGGACGACGAGCCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGG 715
```







```
Qy       3197 GGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTC 3256
             ||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||
Db       3287 GGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCAT 3346

Qy       3257 TGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA 3316
             ||||||| |||||||||| || ||||| ||||||||||||||||||||||||| ||||
Db       3347 TGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA 3406

Qy       3317 CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC 3376
             | ||||||||||||||||| ||||| |||||||| ||||||||||||||||||||||||
Db       3407 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC 3466

Qy       3377 ACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT 3436
             ||||||||||||||||| | |||||||||||||||||| ||||| |||||||||||
Db       3467 ACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGT 3526

Qy       3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCT 3496
             |||||||||||||||||||||||||||| |||| ||||| ||||| ||||| || ||||
Db       3527 ACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCT 3586

Qy       3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATG 3556
             |||||||||||||||||||| |||||||||||||||||||||||| ||||| ||||
Db       3587 TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATG 3646

Qy       3557 TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616
             |||||||||||||| |||||||||||||||||||||| ||||| || ||||||||||||
Db       3647 TTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 3706

Qy       3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676
             |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||| |
Db       3707 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 3766

Qy       3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736
             ||| |||||| ||||| ||||| ||||||||||||||||||||||||||||||||||||
Db       3767 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3826

Qy       3737 CAGA 3740
             | ||
Db       3827 CTGA 3830
```

RESULT 2
US-08-700-607-2
; Sequence 2, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

```
;       STATE:  CA
;       COUNTRY:  U.S.
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  799 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:  Consensus
US-08-700-607-2

  Query Match             13.3%;  Score 497.4;  DB 2;  Length 799;
  Best Local Similarity   92.7%;  Pred. No. 9.2e-106;
  Matches  522;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       3178 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 3237
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        108 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 167

Qy       3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297
              |||||||||||||  ||  ||||||| |||||||||||  ||  |||||  ||||||||||||
Db        168 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 227

Qy       3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
             |||||||||||||| |||||  |||||||||||||||||  |||||  ||||||||  ||||||
Db        228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287

Qy       3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
             |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        288 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347

Qy       3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
             |||||  ||||||||||| |||||||||||||||||||||||||||||||  ||||  |||||
Db        348 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 407

Qy       3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
             |||||  |||||  ||  |||||||||||||||||||||||||  ||||||||||||||||||
Db        408 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 467
```

```
Qy       3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
             |||||||| ||||| |||||||||||||||| |||||||||||||||||||||| |||
Db        468 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 527

Qy       3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
             || || |||||||||||| |||||||||||||||||||||||||  |||||||||||
Db        528 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587

Qy       3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
             |||||||||||||||| |||| |||||| ||||| ||||| ||||||||||||||||||
Db        588 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 647

Qy       3718 CCTGGATTGAAGCGCAAAGCAGA 3740
             |||||||||||||||||||| ||
Db        648 CCTGGATTGAAGCGCAAAGCTGA 670
```

RESULT 3
US-09-149-476-254
; Sequence 254, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.1%; Score 228.8; DB 4; Length 1766;
Best Local Similarity 63.4%; Pred. No. 2.5e-43;
Matches 350; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

Qy 3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGC 3233
Db 286 TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 345

```
Qy       3234 CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACAT 3293
              ||   |  || ||||||| || ||| |||  |||||  |  |||||||     | ||| |
Db        346 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCT 405

Qy       3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
                | |||| || ||||| || || |||||||| ||||| || |||  ||| |||||  ||
Db        406 CATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 465

Qy       3354 TATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
              | | ||||| ||||| |||||||| ||||||| || ||  | ||    ||  || || |
Db        466 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 525

Qy       3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAT 3473
              ||    |||    | || || ||||  ||| ||||  | |  ||  | |||||  |  |
Db        526 GTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 585

Qy       3474 AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGT 3533
              |||    | |  || || ||  | || || ||| | ||||| ||| ||||| | || ||
Db        586 GAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 645

Qy       3534 GTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTT 3593
              || |||||| || | || ||||||||||  | || || ||  | || || || ||| |
Db        646 CTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCT 705

Qy       3594 AGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653
              |||    |     | |||||| | ||  || | |||||   | |  ||   ||||| ||
Db        706 TGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 765

Qy       3654 TCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3713
              ||| ||| | ||  | ||     |       |||      | |  || ||||||||||
Db        766 TCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 825

Qy       3714 AATCCCTGGATT 3725
              | |||||||| |
Db        826 ACTCCCTGGAAT 837
```

RESULT 4
US-09-149-476-255
; Sequence 255, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.1%; Score 228.8; DB 4; Length 2664;
Best Local Similarity 63.4%; Pred. No. 3.1e-43;
Matches 350; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

```
Qy       3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGC 3233
              | | ||    || ||  | | |||||||||  | ||||||||||  | || |||||  |
Db        261 TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 320

Qy       3234 CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACAT 3293
              ||   |  || ||||||| || ||| |||  |||||  |  |||||||     | ||| |
Db        321 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCT 380

Qy       3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
                | |||| || ||||| || || |||||||| ||||| || |||  ||| ||||| ||
Db        381 CATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 440

Qy       3354 TATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
              | | ||||| ||||| |||||||| |||||||  || ||  | ||    ||  || || |
Db        441 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 500

Qy       3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAT 3473
              ||    |||    | || || ||||  ||| ||||  | |  ||  | |||||  |  |
Db        501 GTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 560

Qy       3474 AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGT 3533
              |||    | |  || || ||  | || || ||| | ||||| ||| ||||| | || ||
Db        561 GAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 620

Qy       3534 GTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTT 3593
              || ||||||. || | || ||||||||||  | || || ||  | || || || ||| |
Db        621 CTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCT 680

Qy       3594 AGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653
              |||    |     | |||||| | ||  || | |||||   | |  ||   ||||| ||
Db        681 TGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 740

Qy       3654 TCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3713
              ||| ||| | ||  | ||     |       |||       | |  || ||||||||||
Db        741 TCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 800

Qy       3714 AATCCCTGGATT 3725
              | |||||||| |
Db        801 ACTCCCTGGAAT 812
```

RESULT 5
US-08-700-607-4
; Sequence 4, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THP1NOB01
; CLONE: 31870
US-08-700-607-4

Query Match 5.4%; Score 203.6; DB 2; Length 1095;
Best Local Similarity 61.6%; Pred. No. 1.3e-37;
Matches 337; Conservative 1; Mismatches 208; Indels 1; Gaps 1;

Qy 3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGC 3233
Db 328 TGCGGTGCACGATCTGATTTTMTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 387

Qy 3234 CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACAT 3293
Db 388 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCT 447

```
Qy       3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
Db        448 CATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 507

Qy       3354 TATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
Db        508 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 567

Qy       3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAT 3473
Db        568 GTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 627

Qy       3474 AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGT 3533
Db        628 GAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 687

Qy       3534 GTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTT 3593
Db        688 CTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCT 747

Qy       3594 AGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653
Db        748 TGCTGAACTGCTCATTTTNAGTGTCCCGATTGTNTATNAGAAGTACAAGGTTC-CAAGCA 806

Qy       3654 TCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3713
Db        807 AAACTCCCTGGAATCGCCAAAAAAAAGGCAGAATAAGTACATGGAAACCAGAAATGCAAC 866

Qy       3714 AATCCCT 3720
Db        867 AGTTACT 873
```

RESULT 6
US-09-149-476-102
; Sequence 102, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 4.8%; Score 180.4; DB 4; Length 794;
Best Local Similarity 61.0%; Pred. No. 2.6e-32;
Matches 332; Conservative 6; Mismatches 202; Indels 4; Gaps 3;

```
Qy       3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGC 3233
              | | ||    || ||  | | |||||||||  | ||||||||||  |.|| ||||  |
Db        253 TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTG--GA 310

Qy       3234 CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCC-TACA 3292
              ||   |  || ||||||| || ||| |||  |||||  |  |||:|||      | ||:
Db        311 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCARTGTGGGTTTCTTAMC 370

Qy       3293 TTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGG 3352
              |   | |||| || ||||| || || ||||:||| ||||| || |||  ||| ||||| |
Db        371 TCATCCTGGCTCTTCTCTCTGTCACCATCARCTTCAGGATCTACAAGTCCGTCATCCAAG 430

Qy       3353 CTATCCAGAAATCAGATGAAGGCCACCCATT-CAGGGCATATTTAGAATCTGAAGTTGCT 3411
              || | |||||:||||| :||||||| |||:| ||  || ||  | ||    ||  || ||
Db        431 CTGTWCAGAARTCAGAARAAGGCCATCCAWTCCAAAGCCTACCTGGACGTAGACATTACT 490

Qy       3412 ATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACA 3471
              | ||    |||    | || || ||||  ||| ||||  | |  ||  | |||||  |
Db        491 CTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCC 550

Qy       3472 ATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCA 3531
              | |||    | |  || || ||  | || || ||| | ||||| ||| ||||| | ||
Db        551 CTGAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCT 610

Qy       3532 GTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATT 3591
              || || |||||| || | || |||||||||||  | || || ||  | || || || |||
Db        611 GTCTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATT 670

Qy       3592 TTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATA 3651
              | |||    |      | |||||| | ||  || | |||||   | |  ||   |||||
Db        671 CTTGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATT 730

Qy       3652 GATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCA 3711
              ||||| ||| | ||  | ||     |       |||       | |  || |||| |
Db        731 GATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGC 790

Qy       3712 AAAA 3715
              ||||
Db        791 AAAA 794
```

RESULT 7
US-08-700-607-9
; Sequence 9, Application US/08700607

```
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,607
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0114 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  261 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  SPLNFET01
;      CLONE:  28742
US-08-700-607-9

  Query Match             4.4%;  Score 164.6;  DB 2;  Length 261;
  Best Local Similarity   86.7%;  Pred. No. 6.7e-29;
  Matches  176;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy       3237 CTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGC 3296
              | ||| || |||||| ||  ||||||| |||||||||||| || ||||| ||||||||||
Db          1 CCTATNCCNGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGC 60

Qy       3297 CTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTAT 3356
              ||| ||||||| ||| ||||| ||||||| |||| |||| ||||| |||||||| |||||
Db         61 CTTNGCCCTGCNCTCTGTGACCATCAGCTNTAGGCTATACAAGGGTGTGATCCAAGCTAT 120

Qy       3357 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATC 3416
              |||||||||||||||||| |||||||||||||||||| | || ||||||||||||||||
Db        121 CCAGAAATCAGATGAAGGNCACCCATTCAGGGCATATCTGGANTCTGAAGTTGCTATATC 180
```

```
Qy       3417 AGAGGAATTGGTTCAGAAATACA 3439
              ||||| ||| ||||||| ||||
Db        181 TGAGGAGTTGNTTCAGAAGTACA 203


RESULT 8
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.0%;  Score 75.4;  DB 1;  Length 7218;
  Best Local Similarity   5.3%;  Pred. No. 1.8e-07;
```

```
  Matches   22;  Conservative  242;  Mismatches  153;  Indels    0;  Gaps    0;

Qy       1127 TTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAA 1186
              ||||||       | ||   |   |::  : :  :: :::::: :  :::::::::: ::
Db       1459 TTAAAGAGATAGAAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1400

Qy       1187 TTGTGAGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAG 1246
                : :::::: ::::: ::::::::   ::   : :: : ::      : ::   : :::
Db       1399 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1340

Qy       1247 AATCACCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTA 1306
              ::  :   : ::: :::::::: ::::  : :     :::::::: :: ::: :     :
Db       1339 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1280

Qy       1307 ATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCAT 1366
              : :::: : ::: :  :: :: :: :   : :::::::::: : : :::    :::  :
Db       1279 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1220

Qy       1367 TTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTA 1426
                ::: ::: : :::::: :::::: :   : :::::::: ::::: : :  ::  :  :
Db       1219 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1160

Qy       1427 GAGCTAATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAA 1486
              :::  :: : :::::: :::: ::: :::::: :   :::::: ::   :::: ::::::
Db       1159 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1100

Qy       1487 GTCTTGGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAG 1543
              :    :::::::: :: ::::: ::::: ::::||       ||||  |  |  |||
Db       1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAG 1043


RESULT 9
US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
```

```
  Query Match             2.0%;  Score 75.2;  DB 3;  Length 152331;
  Best Local Similarity   53.8%;  Pred. No. 1e-06;
  Matches  155;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy        463 CCGCCCGCCGCCGCCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCC 522
              || | | || ||| | |||| |    || |  |  |  | | |    ||||||||||||
Db      21936 CCCCGCCCCCCCGGCCCGCCCCCCGCGGCCCCCCACCCCCCCCCCCCCCCCCCGCGCCC 21995

Qy        523 CGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGC 582
              |||   || |  |  ||| | | |||  |||| ||   |   |  ||  ||        |
Db      21996 CGCCCCCCCCCCCCGCGCCCCCCACCCCCCCGCCCCCCCGCCCCCCCCCCCCCCCCCACC 22055

Qy        583 AGCCCCGCGGCGCCCGCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTC 642
                || | |   |||| | |   |||  |  ||||  ||| | | ||  ||| ||  ||
Db      22056 CCCCACACCCGGCCCACACGCACCCCCCACCCCGACGCCCCCGCCCCCCCCCCCCCGCAG 22115

Qy        643 CCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCC 702
              ||   |  |  |   |  ||| |  | ||| | || ||| | ||  ||| |||    |||
Db      22116 CCGACGCCCCCCCCCCGCCCGCCCCGCCCCGCACCCCCGACCCCCCCCCGCCGCCCCGCCC 22175

Qy        703 CTGGCGGAGCCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
              | | |    ||| |||  |||||  || |    || |||||| | | |
Db      22176 CCGCCCCCCCCCCCCCGGCCCCCCCCCCGCCGGCGCGGCGCCCCACCCC 22223


RESULT 10
US-09-894-998A-35/c
; Sequence 35, Application US/09894998A
; Patent No. 6537555
; GENERAL INFORMATION:
;  APPLICANT: Hosken, Nancy Ann
;  APPLICANT:  Craig H. Day
;  APPLICANT:  Davin C. Dillon
;  APPLICANT:  McGowan, Patrick
;  APPLICANT:  Sleath, Paul R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
;  FILE REFERENCE: 210121.538
;  CURRENT APPLICATION NUMBER: US/09/894,998A
;  CURRENT FILING DATE:  2001-06-28
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 2481
;   TYPE: DNA
;   ORGANISM: HSV-2
US-09-894-998A-35

  Query Match             2.0%;  Score 74.6;  DB 4;  Length 2481;
  Best Local Similarity   48.7%;  Pred. No. 1.6e-07;
  Matches  203;  Conservative    0;  Mismatches  214;  Indels    0;  Gaps    0;

Qy        327 GTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGGAGGAGGACGAGGA 386
              | ||  |  || ||||   ||    | |  |   |  ||||| |||| |||||| |||||
Db       1920 GGACGCGGACGCGACGCTCCCACCAGCCCCGCCCGCAGAGGAAGAGGCGGAGGAGGAGGA 1861
```

```
Qy        387 GGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGCCCGCAGCCGGGCT 446
              || ||| || |||||    |||||   ||||| |  |||| | || | |  |  | |
Db       1860 GGCGGAGGAGGAGGAGGCGGAGGAGGAGGAGGCGGAGGAGGAGGAGGCGGAGGAGGAGGA 1801

Qy        447 GTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCGCCGCTGCTGGACTTCAGCAGCGACTC 506
              | | |  |  | || | ||   |  |  |  ||| ||  |   |    | |   ||||
Db       1800 GGCGGAGGAGGAGGAGGCGGAGGAGGAGGAGGCGGCGGCGACCGCGGCCTGGGACGACGG 1741

Qy        507 GGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCA 566
               |   ||  || |  |   | |||   |   |||| | |    | | |       | ||
Db       1740 AGACGCCGACGGGGGCGCGGCGCCCGCGGACGCCGGGGCGAGCGGCCCGTGGCCGCGGTC 1681

Qy        567 GCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGCCCGCTGCCGCAGT 626
              |||    |  ||   | |  ||  |      |||  |   | || | ||| |  ||   |
Db       1680 GCCCGAGTCCGAGTCCGGGGCCCGGCGCGGCGCCGCCCTCTTGGCCCCCACCCCCTGGGG 1621

Qy        627 CCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCC 686
                |     | ||| |   | ||  || ||     ||| |       |  |   |||
Db       1620 GGCGAGGGGCGAGCGCGGGGCGGCGGAGGAAGAGGCGGAGGACGAGGCCGCGGGGCCCGA 1561

Qy        687 AGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGCCGGCCGCGCC 743
               ||| | || ||| | |   || ||  |||||  |||| ||| || ||   | | |
Db       1560 GTCCGACCCGCGCCTCTTCCGGGGGCGGGCCGCCGCCCCCTCCGCGGCGTGGGGGGC 1504
```

RESULT 11
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.0%; Score 73.2; DB 3; Length 4403765;
Best Local Similarity 52.3%; Pred. No. 1.8e-05;
Matches 162; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

```
Qy        434 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCGCCGCTGCTGGACT 493
              |||   | | |||| ||||  |  ||| ||||||     |  | | |||||  | |
```

```
Db    3926346 CCGTGCCGGCGCTGCCCGCGCCGCCGGCGCCGCCTTGGCCGCCGGTGCCGCCGATACCGG
3926287

Qy        494 TCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553
              |     ||   ||  | |  || ||||       ||| ||||||| || || || |||
Db    3926286 CCTTGCCCGCGGCGCCGACAACCCCGCCGGTTCCTCCGGTGCCGGCGGCCCCGCCGGCCC
3926227

Qy        554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613
              | || | |  |  |  | |    | |    | |  || || | ||||||  || || |
Db    3926226 CGCCGGCGCCGGCGTTACCGCCAGTCCCACCCGCGCCGCCGTCGGCGCCAATCCCGCTGG
3926167

Qy        614 CCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673
              |     | |||     |||  ||| ||  || | |        ||| |||| |  |||
Db    3926166 CATTATCAGCACCGGAGCCACCCATGCCGCCGGCGCCGCCTTGGCCGCCGGTGCCGCCGG
3926107

Qy        674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733
              | || |||  |||        ||    | |||||  |||  ||  ||| ||  |  |||
Db    3926106 CACCACCGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCTGGCCGCCGACGCCGC
3926047

Qy        734 CGGCCGCGCC 743
              ||||| ||||
Db    3926046 CGGCCCCGCC 3926037


RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             2.0%;  Score 73.2;  DB 3;  Length 4411529;
  Best Local Similarity   52.3%;  Pred. No. 1.8e-05;
  Matches  162;  Conservative    0;  Mismatches  148;  Indels    0;  Gaps    0;

Qy        434 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCGCCGCTGCTGGACT 493
              |||   | | |||| ||||  |  ||| ||||||     |  | | ||||| | |
```

```
Db    3932558 CCGTGCCGGCGCTGCCCGCGCCGCCGGCGCCGCCTTGGCCGCCGGTGCCGCCGATACCGG
3932499

Qy        494 TCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553
              |     ||   ||  | |  || ||||       ||| ||||||| || || || |||
Db    3932498 CCTTGCCCGCGGCGCCGACAACCCCGCCGGTTCCTCCGGTGCCGGCGGCCCCGCCGGCCC
3932439

Qy        554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613
              | || | |  |  |  | |    |  |    | |  || || | ||||||  || || |
Db    3932438 CGCCGGCGCCGGCGTTACCGCCAGTCCCACCCGCGCCGCCGTCGGCGCCAATCCCGCTGG
3932379

Qy        614 CCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673
              |     | |||     |||  ||| ||  || | |        ||| |||| |  |||
Db    3932378 CATTATCAGCACCGGAGCCACCCATGCCGCCGGCGCCGCCTTGGCCGCCGGTGCCGCCGG
3932319

Qy        674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733
              | || |||  |||        ||    |  |||||  |||  ||  |||  ||  |  |||
Db    3932318 CACCACCGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCTGGCCGCCGACGCCGC
3932259

Qy        734 CGGCCGCGCC 743
              ||||| ||||
Db    3932258 CGGCCCCGCC 3932249


RESULT 13
US-09-165-264-8/c
; Sequence 8, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
;  APPLICANT:  Vinayagamoorthy, Thuraiayah
;  TITLE OF INVENTION:  Multi-Loci Genomic Analysis
;  FILE REFERENCE:  44747
;  CURRENT APPLICATION NUMBER: US/09/165,264
;  CURRENT FILING DATE:  1998-10-01
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 319
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-8

  Query Match             1.8%;  Score 68.6;  DB 3;  Length 319;
  Best Local Similarity   52.2%;  Pred. No. 1.3e-06;
  Matches  152;  Conservative    0;  Mismatches  139;  Indels    0;  Gaps    0;

Qy        454 GCTGCGGTGCCGCCCGCCGCCGCCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCC 513
              |||||  |  || ||| || || || | || |  |    |  |  |  |  | |    |||
Db        308 GCTGCAGACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 249

Qy        514 CCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCC 573
```

```
                ||| | |||| |   || |  ||  || | |||||  || | ||       |  ||  ||
Db        248 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 189

Qy        574 TGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCC 633
                  | |  |||| |  | ||| | ||  |||  || ||| |  || |   ||  |||
Db        188 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 129

Qy        634 TCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGC 693
                ||   | |||      |  |   || ||  |    ||||| || || || ||  ||  |
Db        128 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 69

Qy        694 GCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCC 744
                |   |||||   |    ||| || | |||||  || | ||  || | |||
Db         68 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 18


RESULT 14
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             1.8%;  Score 68;  DB 3;  Length 4403765;
  Best Local Similarity   48.9%;  Pred. No. 0.00029;
  Matches  216;  Conservative    0;  Mismatches  220;  Indels    6;  Gaps    1;

Qy        302 CGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGG 361
              || | | |    |||| ||  ||  |   || | |     || ||  | ||||  || ||
Db    3925703 CGGCGCCGGTGGCGCCGGCGGTCGCGGCGCACTGCTGCTGGGCGCTGGCGGACAGGGCGG
3925762

Qy        362 ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC 421
               |  || || |  || |||| ||| ||     |  | |      |||     |     |
Db    3925763 CCTCGGCGGCGCCGGCGGACAAGGCGGCACCGGCGGGGCCGGCGGAGATGGCGTTCTGGG
3925822

Qy        422 TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCGC 481
```

```
                 || |  |  | |    |  |    | | |   | |||| |  ||  ||| | || | ||
Db    3925823 GGGTGTCGGTGGCACTGGTGGTAAGGGCGGTGTCGGCGGCGTGGCTGGCCTCGGCGGGGC
3925882

Qy        482 CGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCG 541
              || || ||         ||||   || | |||    ||||  || | |||| ||  |   |
Db    3925883 CGGTGGTGCCGCGGGCCAGCTCTTCAGCGCCGGAGGCGCGGCGGGTGCCGTTGGGGTTGG
3925942

Qy        542 CGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGC 601
              || | || || ||    | | ||| | |      ||| ||     |  || ||||| |||
Db    3925943 CGGCACCGGCGGCCAGGGTGGGGCTGGCGGTGCCGGAGCGGCCGGCGCCGACGCCCCCGC
3926002

Qy        602 CATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTC 661
              || | | |      |      | ||  | ||      |||  | | |   |  | | |
Db    3926003 CAGCACAG------GTCTAACCGGTGGTACCGGGTTCGCTGGCGGGGCCGGCGGCGTCGG
3926056

Qy        662 CGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGC 721
              |||| ||| |  |  | ||   ||| || |   | |   | | || || ||| || || |
Db    3926057 CGGCCAGGGCGGCAACGCCATTGCCGGCGGCATCAACGGCTCCGGTGGTGCCGGCGGCAC
3926116

Qy        722 CCCCTTCCACGCCGGCCGCGCC 743
              |  |  ||| | ||||  || |
Db    3926117 CGGCGGCCAAGGCGGCGCCGGC 3926138
```

RESULT 15
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match   1.8%; Score 68; DB 3; Length 4411529;
  Best Local Similarity   48.9%; Pred. No. 0.00029;
  Matches 216; Conservative   0; Mismatches 220; Indels   6; Gaps   1;

```
Qy        302 CGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGG 361
```

```
                ||  |  | |     ||||  ||   ||   |    ||  |  |       ||  ||   |  ||||   ||  ||
Db    3931915 CGGCGCCGGTGGCGCCGGCGGTCGCGGCGCACTGCTGCTGGGCGCTGGCGGACAGGGCGG
3931974

Qy        362 ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC 421
                |   ||  ||  |   ||  ||||  |||  ||       |   |  |        |||       |      |
Db    3931975 CCTCGGCGGCGCCGGCGGACAAGGCGGCACCGGCGGGGCCGGCGGAGATGGCGTTCTGGG
3932034

Qy        422 TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCGC 481
                ||  |   |   |  |     |   |     |  |  |    |  ||||  |   ||   |||  |  ||  |  ||
Db    3932035 GGGTGTCGGTGGCACTGGTGGTAAGGGCGGTGTCGGCGGCGTGGCTGGCCTCGGCGGGGC
3932094

Qy        482 CGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCG 541
                ||  ||  ||          ||||    ||  |  |||     ||||   ||  |  ||||  ||   |    |
Db    3932095 CGGTGGTGCCGCGGGCCAGCTCTTCAGCGCCGGAGGCGCGGCGGGTGCCGTTGGGGTTGG
3932154

Qy        542 CGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGC 601
                ||  |  ||  ||  ||     |  |  |||  |  |       |||  ||       |   ||  |||||  |||
Db    3932155 CGGCACCGGCGGCCAGGGTGGGGCTGGCGGTGCCGGAGCGGCCGGCGCCGACGCCCCCGC
3932214

Qy        602 CATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTC 661
                ||  |  |  |       |       |  ||   |  ||       |||   |  |  |    |   |  |  |
Db    3932215 CAGCACAG------GTCTAACCGGTGGTACCGGGTTCGCTGGCGGGGCCGGCGGCGTCGG
3932268

Qy        662 CGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGC 721
                ||||  |||  |   |   |  ||    |||  ||  |    |  |    |  |  ||  ||  |||  ||  ||  |
Db    3932269 CGGCCAGGGCGGCAACGCCATTGCCGGCGGCATCAACGGCTCCGGTGGTGCCGGCGGCAC
3932328

Qy        722 CCCCTTCCACGCCGGCCGCGCC 743
                |   |   |||  |  ||||   ||  |
Db    3932329 CGGCGGCCAAGGCGGCGCCGGC 3932350


Search completed: January 23, 2004, 15:31:20
Job time : 202.668 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:28:33 ; Search time 1125.66 Seconds
(without alignments)
11885.997 Million cell updates/sec

Title: US-09-830-972-1
Perfect score: 3741
Sequence: 1 attgctcgtctgggcggcgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2356869 seqs, 1788235258 residues

Total number of hits satisfying chosen parameters: 4713738

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
5 Listing first 45 s mmaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

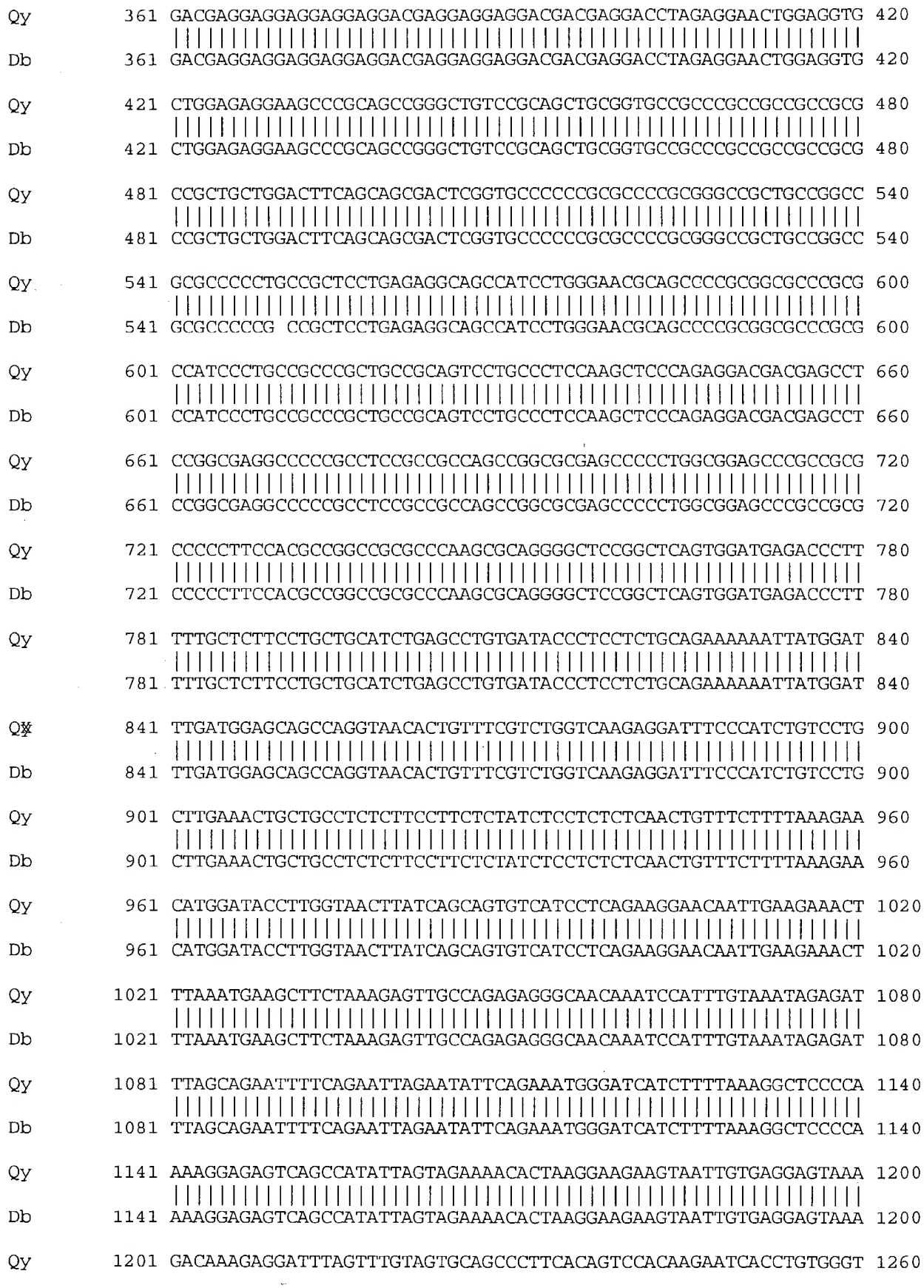
Result No.	Score	% Query Match	Length	DB	ID	Description

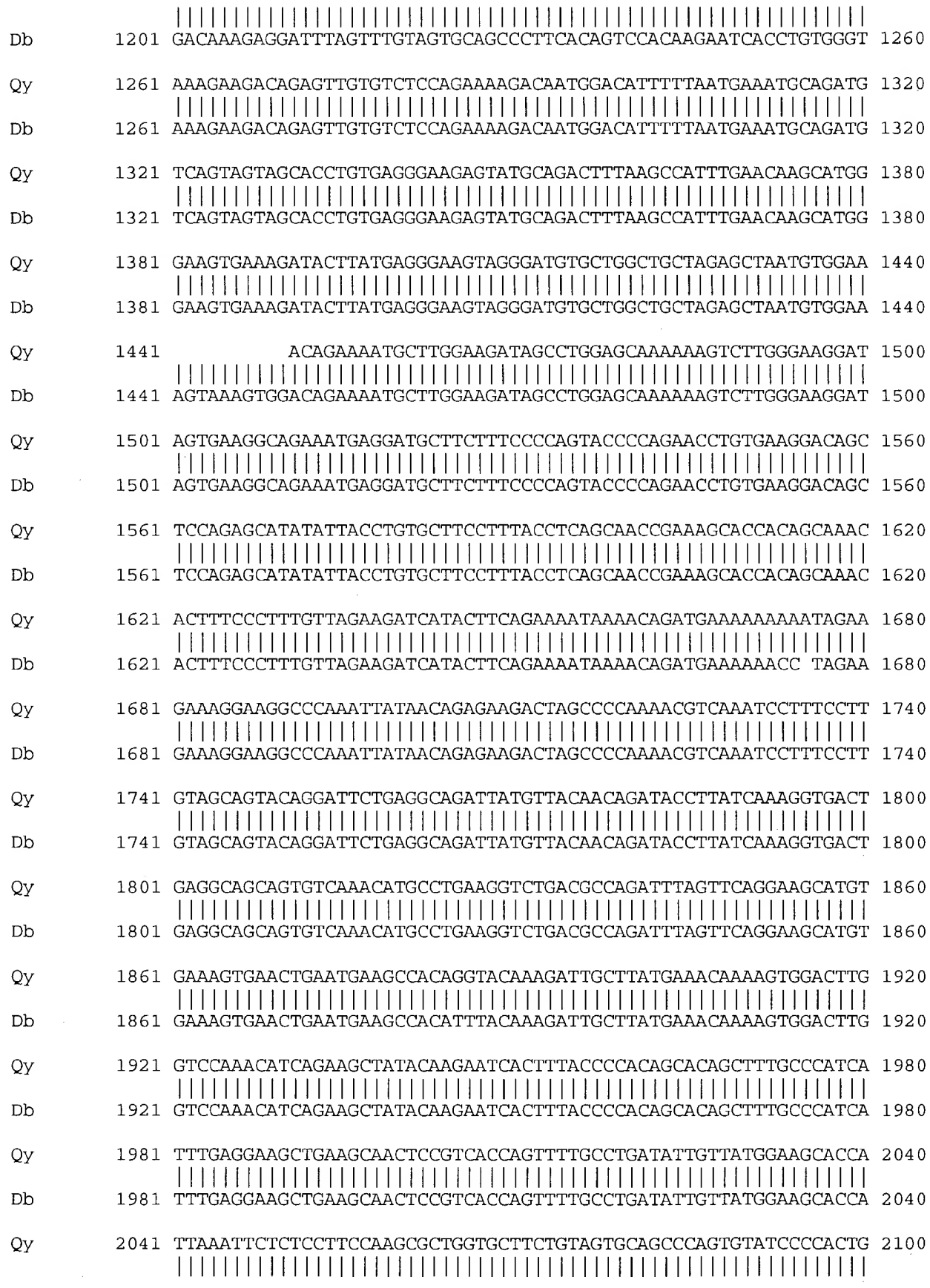
1	3739.4	100.0	4684	9	US-09-893-348-17	Sequence 17, Appl
2	2343.6	62.6	4053	9	US-09-758-140-5	Sequence 5, Appli
3	2343.6	62.6	4053	9	US-09-972-599A-5	Sequence 5, Appli
4	2343.6	62.6	4632	15	US-10-060-036-53	Sequence 53, Appl
5	2289.2	61.2	3579	9	US-09-789-386-1	Sequence 1, Appli
6	2289.2	61.2	3579	9	US-09-893-348-22	Sequence 22, Appl
7	1088.8	29.1	1980	13	US-10-220-891-22	Sequence 22, Appl
8	809.8	21.6	2782	13	US-10-205-194-165	Sequence 165, App
9	497.4	13.3	1122	9	US-09-789-386-5	Sequence 5, Appli
10	497.4		1160	15	US-10-175-523-156	Sequence 156, App
11	497.4	13.3	1785	12	US-10-439-388-62	Sequence 62, Appl
12	497.4	13.3	2235	15	US-10-060-036-54	Sequence 54, Appl
13	495.8	13.3	1610	9	US-09-765-205-5	Sequence 5, Appli
14	483.6	12.9	868	9	US-09-789-386-3	Sequence 3, Appli
15	375.6	10.0	422	10	US-09-960-352-8477	Sequence 8477, Ap
16	374	10.0	422	10	US-09-960-352-11567	Sequence 11567, A
17	322.4	8.6	389	10	US-09-960-352-5154	Sequence 5154, Ap
18	302.6	8.1	423	10	US-09-960-352-9092	Sequence 9092, Ap
19	266.4	7.1	668	12	US-10-264-237-163	Sequence 163, App
20	254	6.8	1520	15	US-10-084-817-333	Sequence 333, App
21	253.2	6.8	3202	10	US-09-954-456-210	Sequence 210, App
22	249.2	6.7	431	10	US-09-960-352-2205	Sequence 2205, Ap
23	244.4	6.5	1502	13	US-10-205-219-94	Sequence 94, Appl
24	242.4	6.5	1473	13	US-10-205-194-128	Sequence 128, App
25	231.8	6.2	3637	12	US-10-108-260A-449	Sequence 449, App
26	231.8	6.2	3637	12	US-10-159-563-443	Sequence 443, App
27	228.8	6.1	1330	15	US-10-106-698-1945	Sequence 1945, Ap
28	228.8	6.1	1656	9	US-09-729-674-19	Sequence 19, Appl
29	228.8	6.1	1668	9	US-09-765-205-25	Sequence 25, Appl
30	228.8	6.1	1766	11	US-09-809-391-254	Sequence 254, App
31	228.8	6.1	1766	13	US-09-882-171-254	Sequence 254, App
32	228.8	6.1	2664	11	US-09-809-391-255	Sequence 255, App
33	228.8	6.1	2664	13	US-09-882-171-255	Sequence 255, App
34	194.4	5.2	489	11	US-09-918-995-15830	Sequence 15830, A
35	190.4	5.1	639	10	US-09-880-107-3484	Sequence 3484, Ap
36	180.4	4.8	794	11	US-09-809-391-102	Sequence 102, App
37	180.4	4.8	794	13	US-09-882-171-102	Sequence 102, App
38	174	4.7	198	9	US-09-758-140-19	Sequence 19, Appl
39	174	4.7	198	9	US-09-972-599A-19	Sequence 19, Appl
40	174	4.7	198	9	US-09-972-599A-21	Sequence 21, Appl
41	170.2	4.5	3413	14	*p21126X201-843-61	Sequence 61, Appl
42	153.4	4.1	330	14	US-10-040-739-366	Sequence 366, App
43	134.4	3.6	573	13	US-10-101-510-401	Sequence 401, App
44	132.8	3.5	259	10	US-09-960-352-13803	Sequence 13803, A
45	126.8	3.4	406	10	US-09-960-352-2239	Sequence 2239, Ap

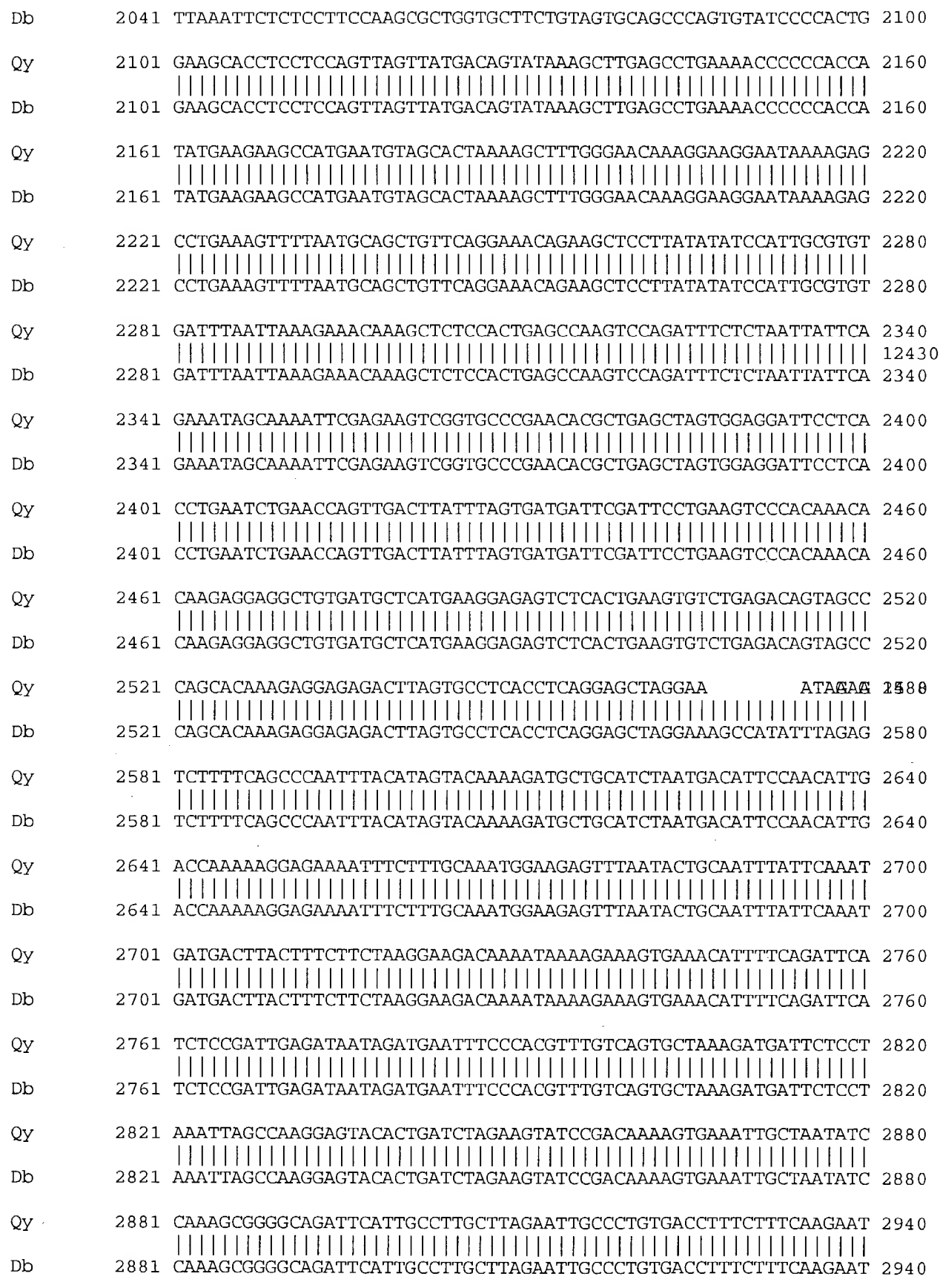
ALIGNMENTS

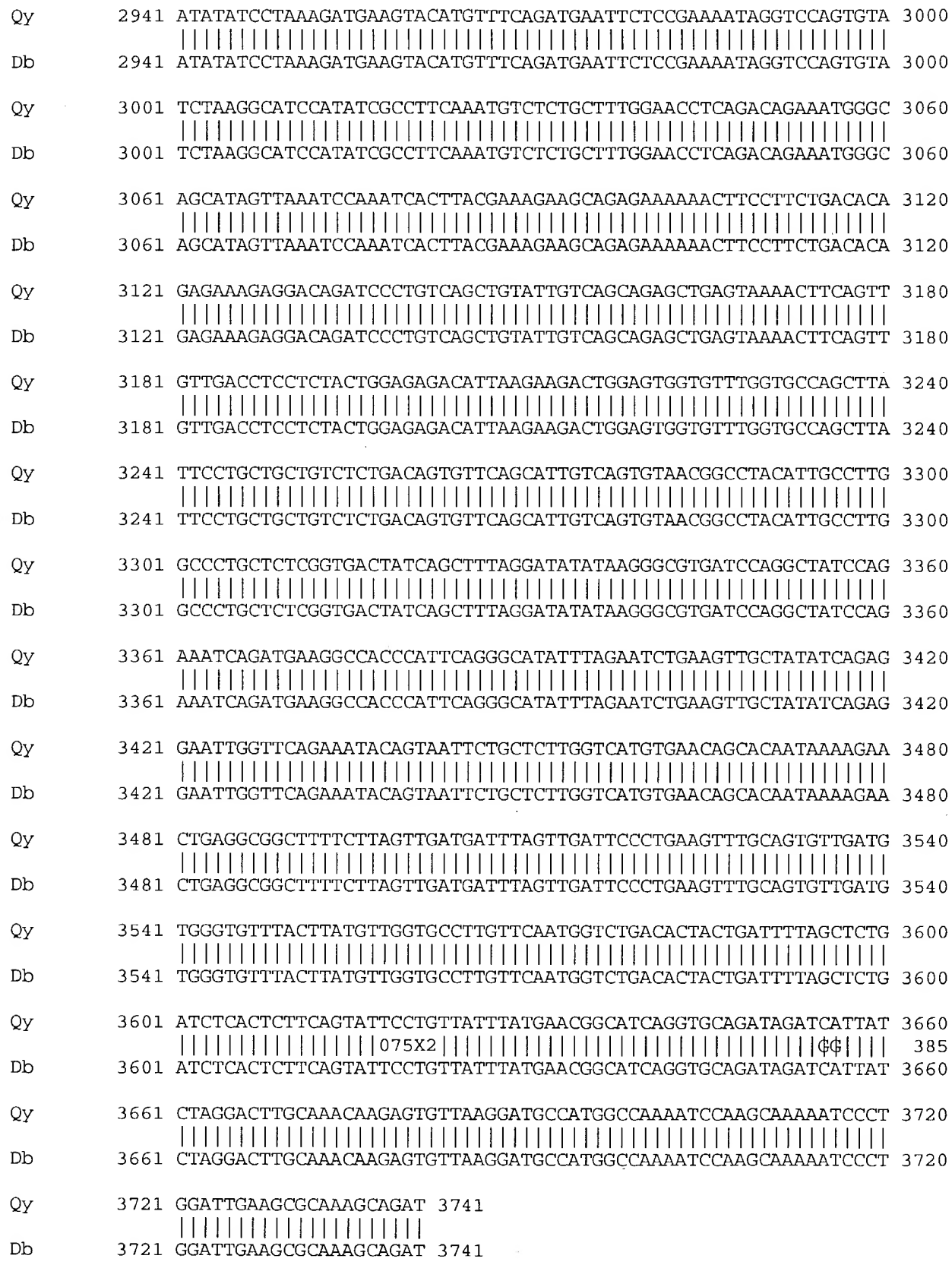
RESULT 1
US-09-893-348-17
; Sequence 17, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal

```
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 4684
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (253)..(3744)
;   OTHER INFORMATION:
US-09-893-348-17

  Query Match             100.0%;  Score 3739.4;  DB 9;  Length 4684;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3740;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60

Qy         61 ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120

Qy        121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCA¢  180

Qy        181 ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240

Qy        241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300

Qy        301 CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGCCCCGGCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
```





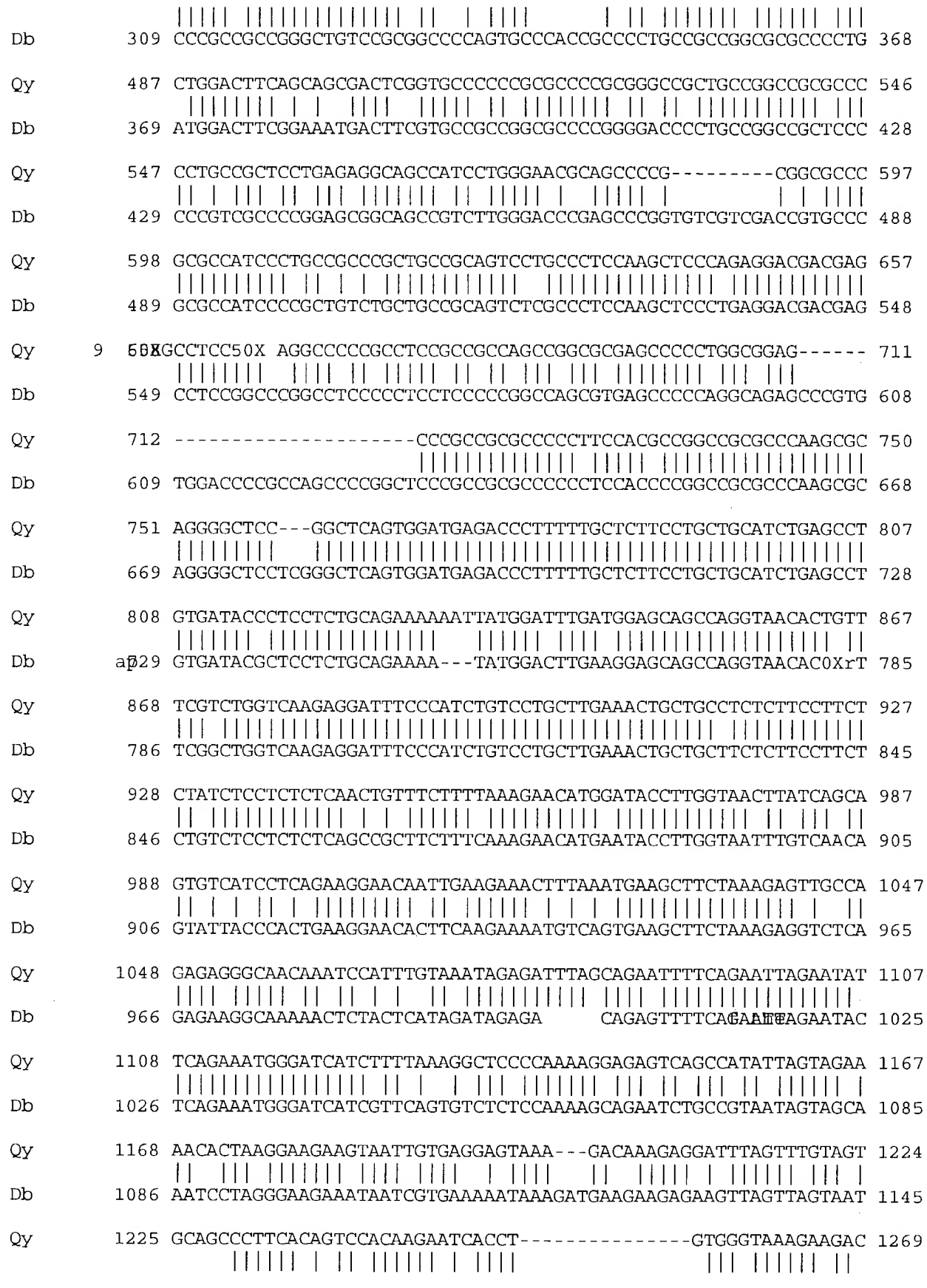


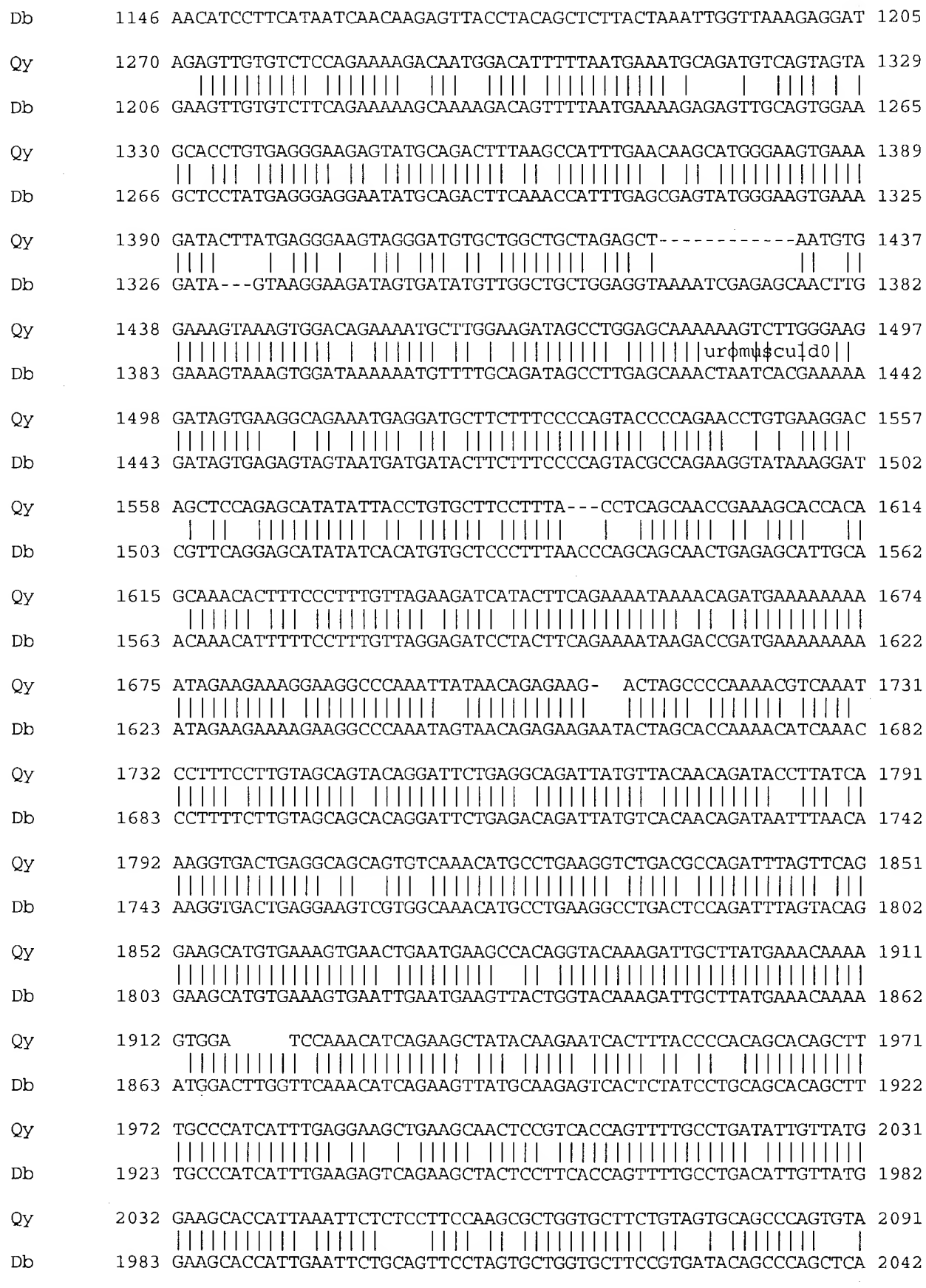

Qy 2941 ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA 3000
Db 2941 ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA 3000
Qy 3001 TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC 3060
Db 3001 TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC 3060
Qy 3061 AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA 3120
Db 3061 AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA 3120
Qy 3121 GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT 3180
Db 3121 GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT 3180
Qy 3181 GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA 3240
Db 3181 GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA 3240
Qy 3241 TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG 3300
Db 3241 TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG 3300
Qy 3301 GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG 3360
Db 3301 GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG 3360
Qy 3361 AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG 3420
Db 3361 AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG 3420
Qy 3421 GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA 3480
Db 3421 GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA 3480
Qy 3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG 3540
Db 3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG 3540
Qy 3541 TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG 3600
Db 3541 TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG 3600
Qy 3601 ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT 3660
075X2 ¢¢ 385
Db 3601 ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT 3660
Qy 3661 CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT 3720
Db 3661 CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT 3720
Qy 3721 GGATTGAAGCGCAAAGCAGAT 3741
Db 3721 GGATTGAAGCGCAAAGCAGAT 3741

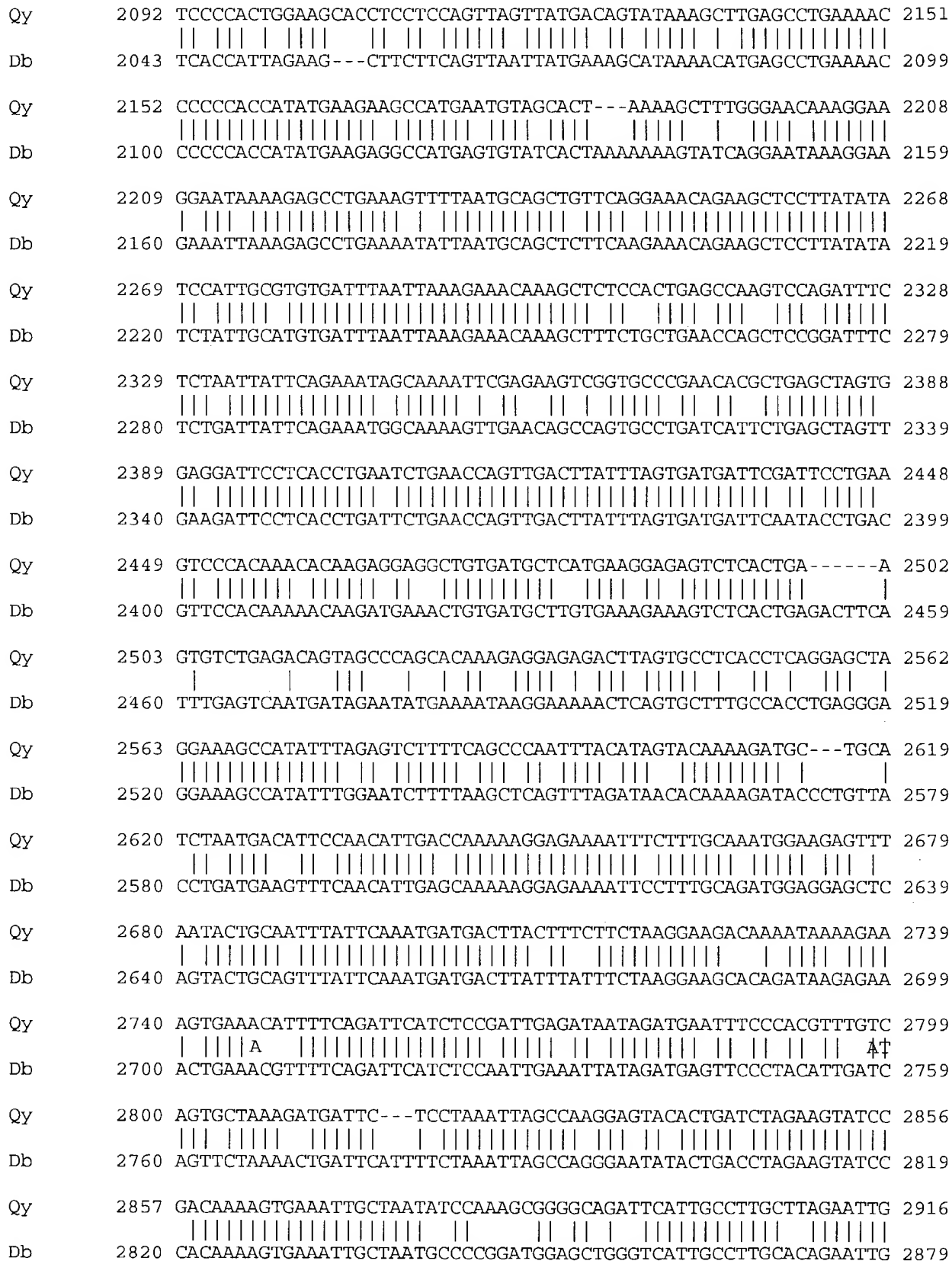
RESULT 2
US-09-758-140-5
; Sequence 5, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human mRNA for No. US20020012965AAo protein (KIAA0886, GenBank
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)
US-09-758-140-5

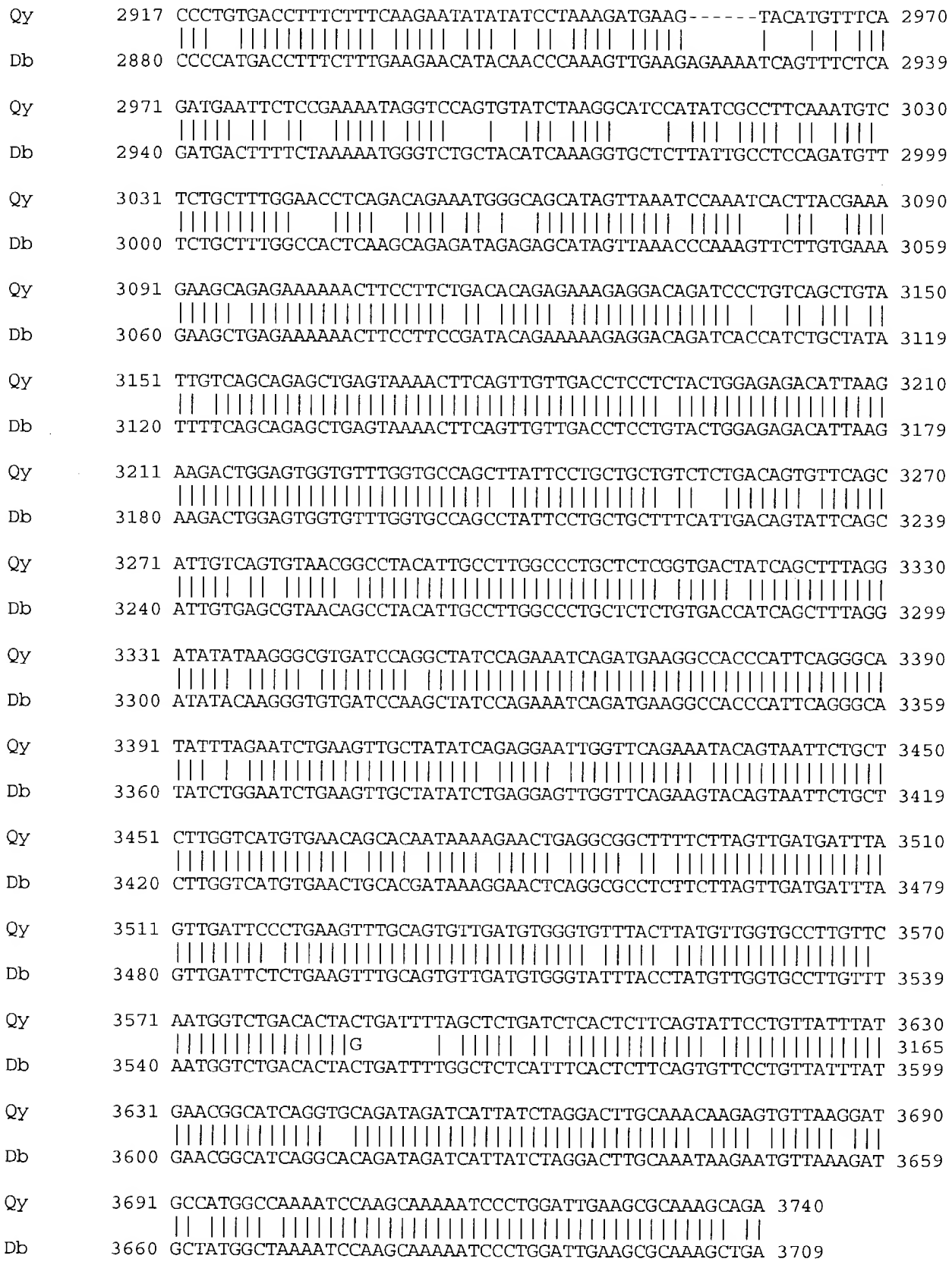
Query Match 62.6%; Score 2343.6; DB 9; Length 4053;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

```
Qy        134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
              | || ||| | | |||  ||||||  ||||| | ||||||||||||||||||||||| ||
Db         16 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 75

Qy        194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
              |||||  |  ||  |  | |||||||| | ||||||||||||  ||  | |||| ||||||
Db         76 CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134

Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
              |||||||||  | ||AGTTGCT | |||||   ||||        ||||||  ||||||||
Db        135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 191

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| |||||||||||||||||| |||||||||||||||||    || || |||
Db        192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        249 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486
```





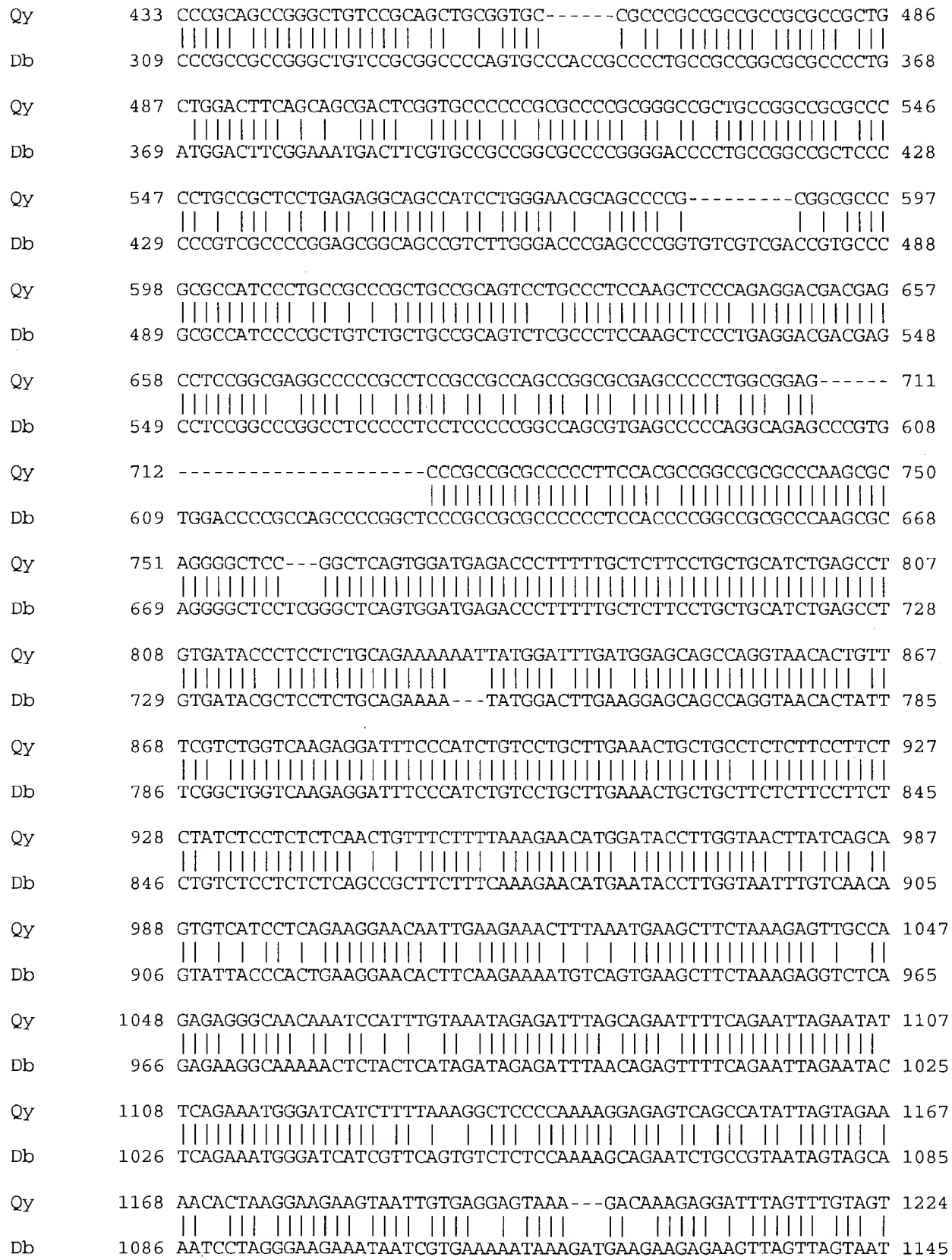


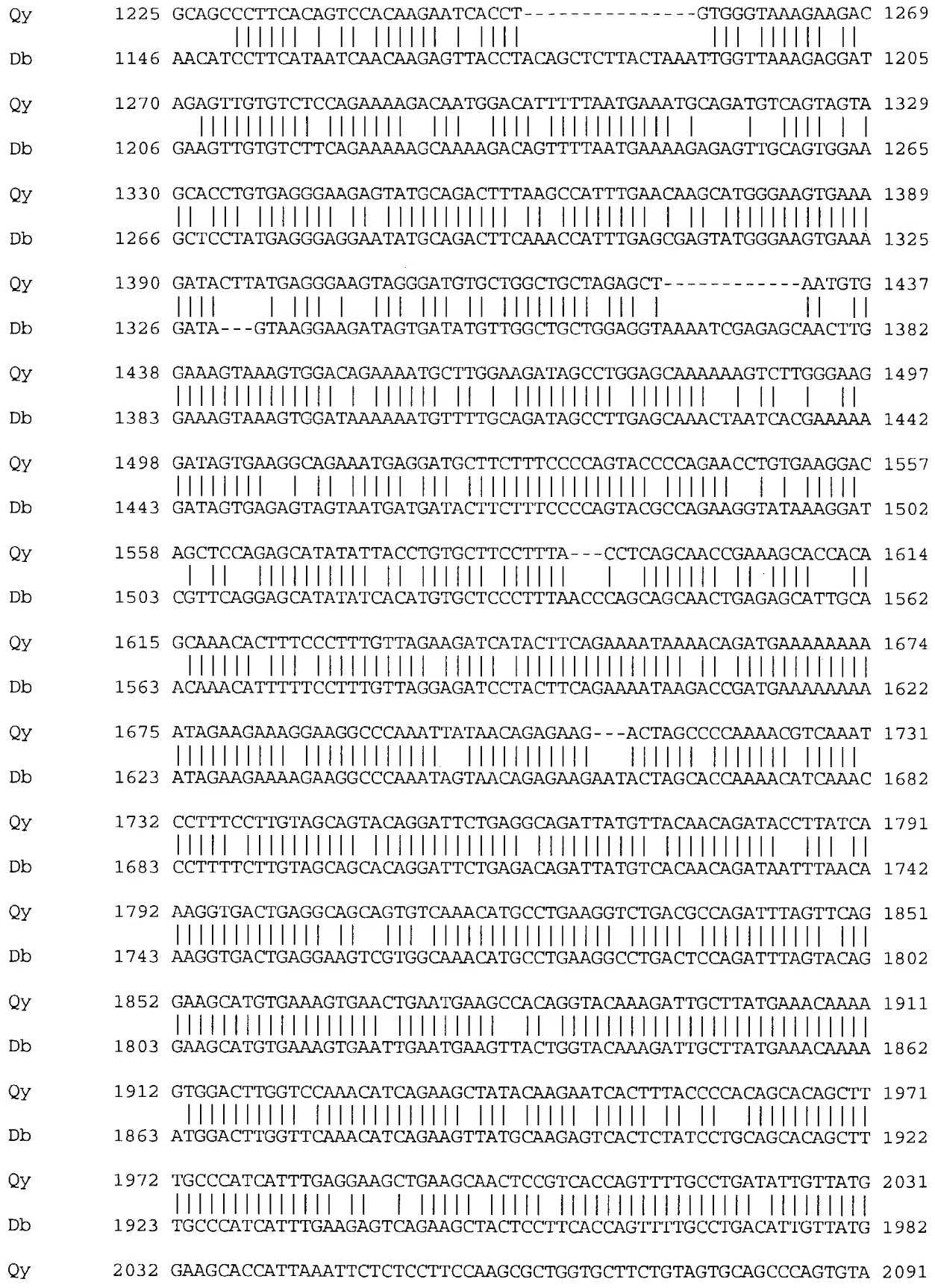


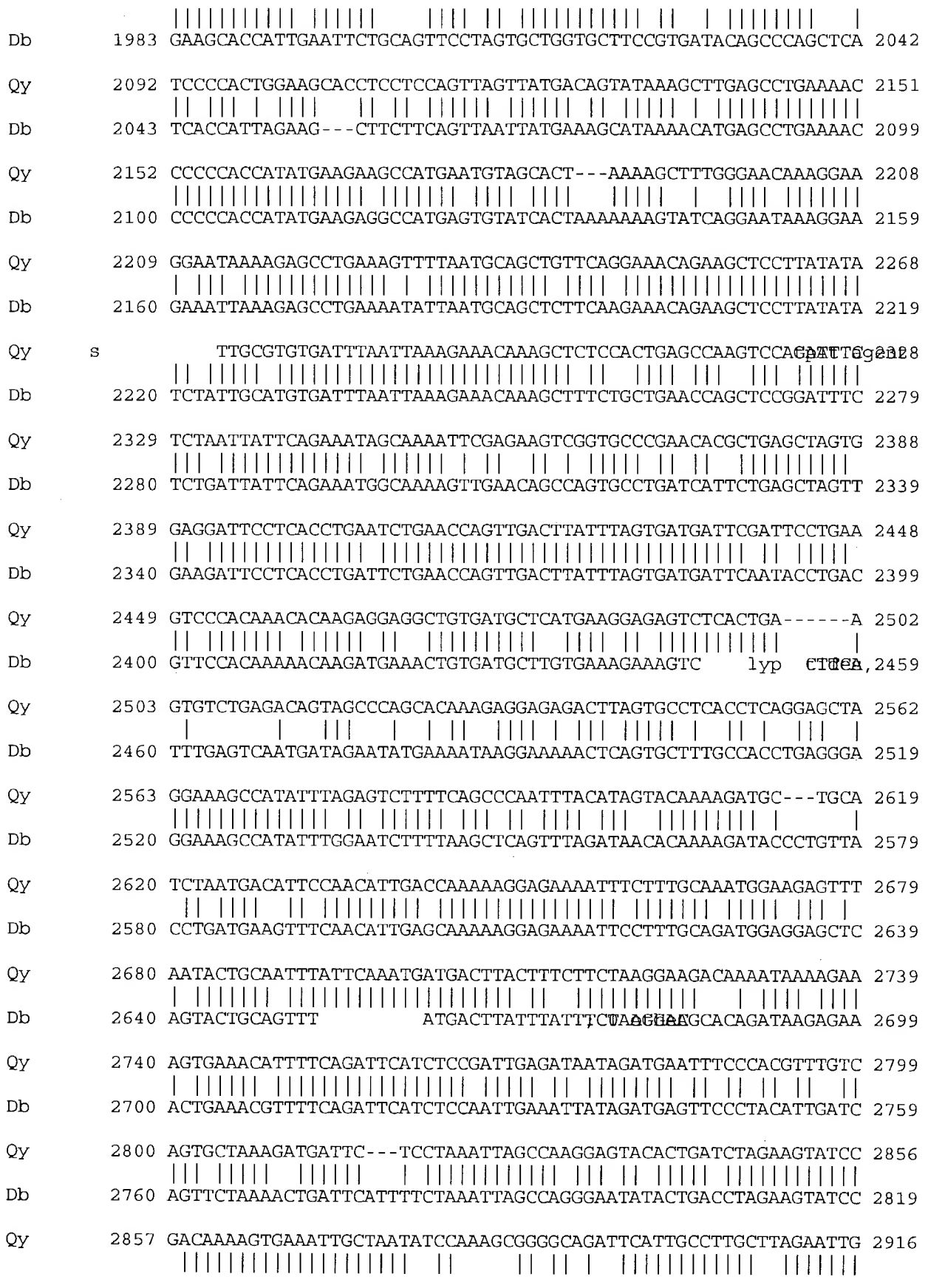
RESULT 3
US-09-972-599A-5
; Sequence 5, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 4053
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (135)..(3710)
;   OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein
(KIAA0886, GenBank
;   OTHER INFORMATION: Accession No. US20020077295A1 AB020693)
US-09-972-599A-5

  Query Match 62.6%; Score 2343.6; DB 9; Length 4053;
  Best Local Similarity 81.3%; Pred. No. 0;
  Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

```
Qy        134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
              | || ||| | | |||  ||||||  ||||| | ||||||||||||||||||||||| ||
Db         16 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 75

Qy        194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
              |||||  |  ||  |  | |||||||| | |||||||||||| ||  | |||| ||||||
Db         76 CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134
           3 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTAGGAGATGGAGAGCCCGCCCCGGCGT 312

              |||||||| | ||||||||  | |||||   ||||||| |||||||||| ||||||||
Db        135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 191

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| |||||||||||||||||| |||||||||||||||||||   || || |||
Db        192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        249 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308
```





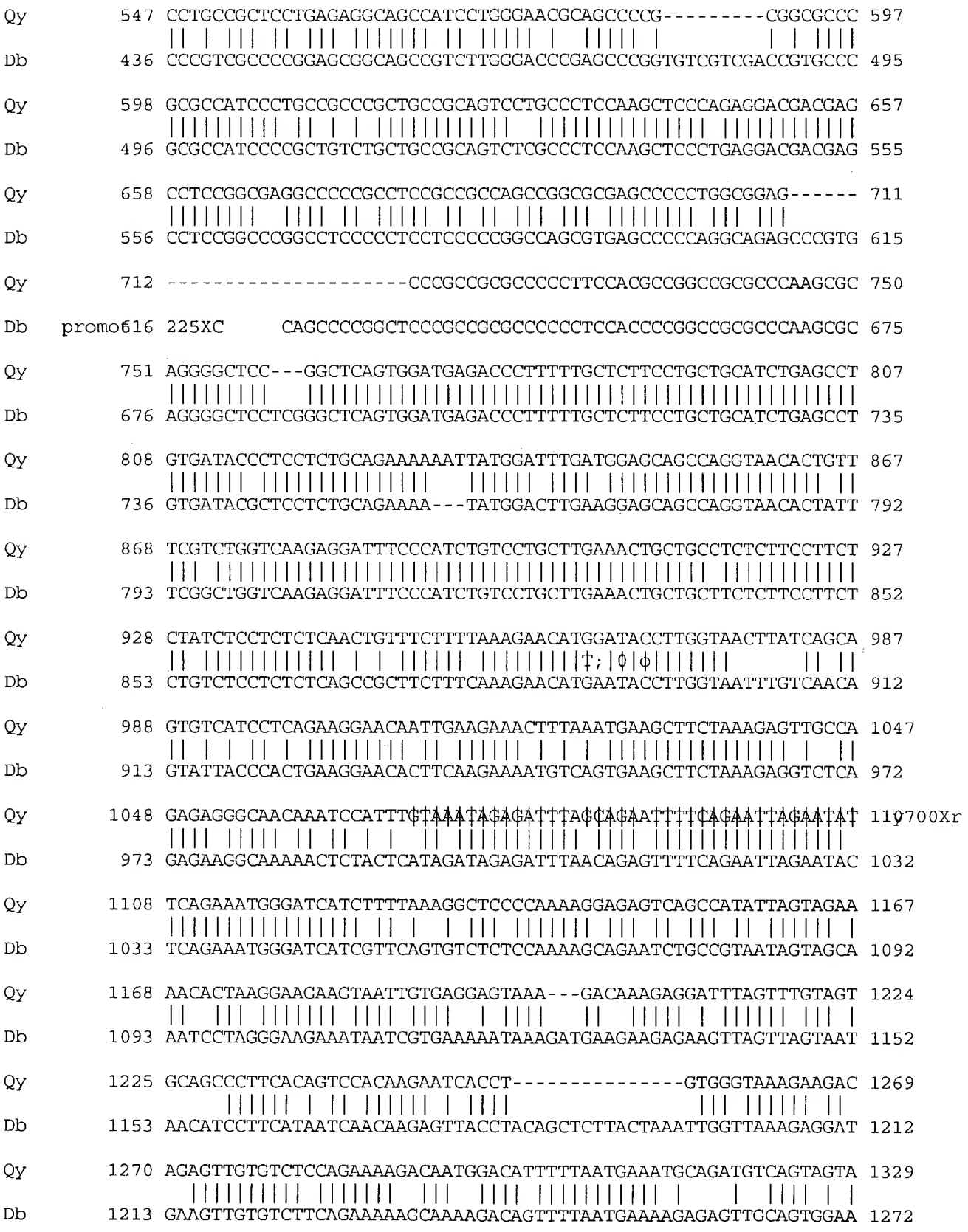


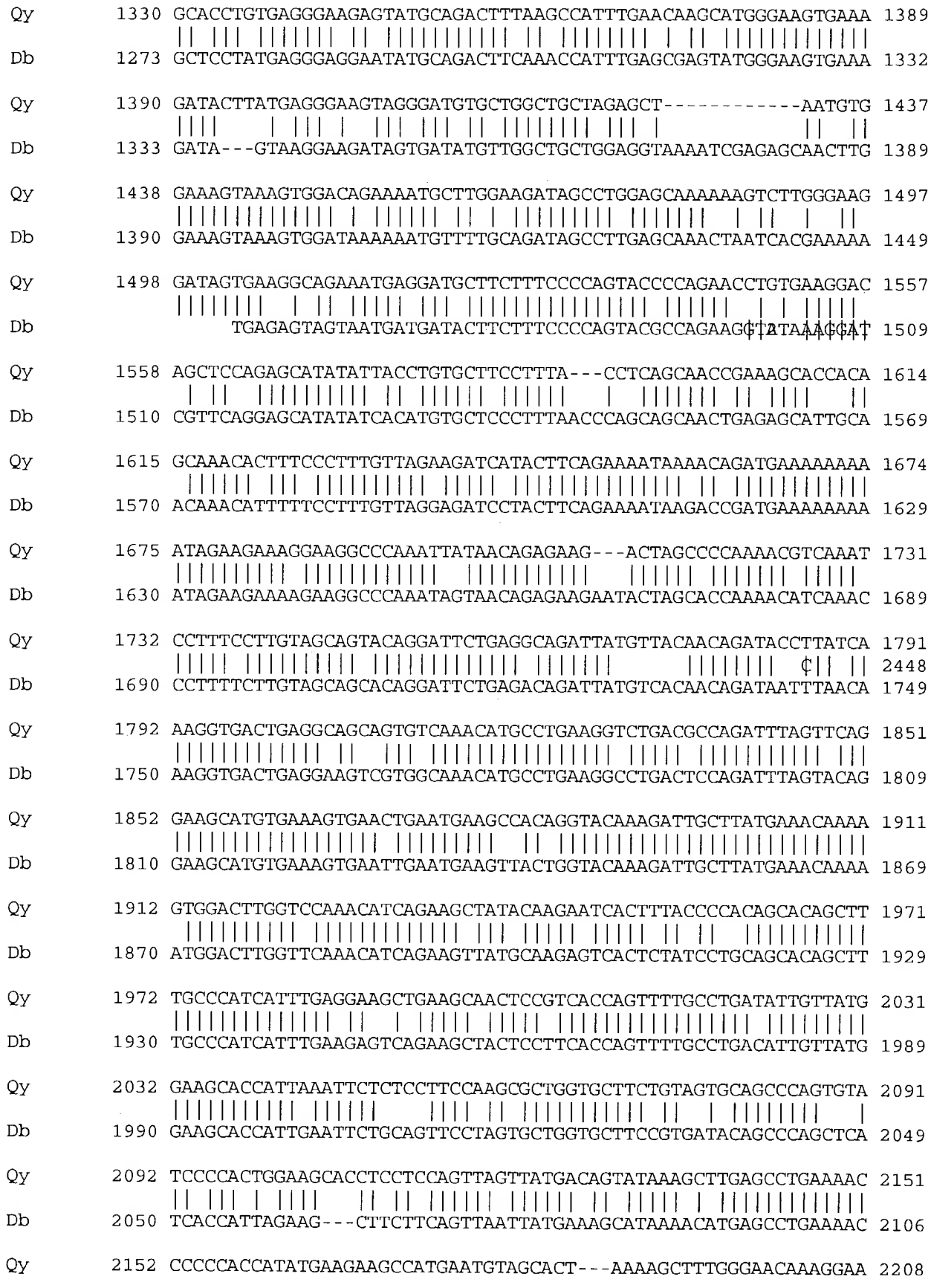
```
Db       2820 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTG 2879

Qy       2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG------TACATGTTTCA 2970
              |||  |||||||||||| ||||| ||| | || |||| |||||      |   | | |||
Db       2880 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2939

Qy       2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
              ||||| || ||  ||||| ||||   |  ||| ||||    | ||| |||| || ||||
Db       2940 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2999

Qy       3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
              ||||||||||   ||||  |||| || |  |||||||||||| |||||   |||  ||||
Db       3000 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 3059

Qy       3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150
              ||||| ||||||||||||||||| || ||||| |||||||||||||| |  || ||| ||
Db       3060 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 3119

Qy       3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
              || ||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       3120 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3179

Qy       3211 AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3270
              |||||||||||||||||||||||||| |||||||||||| ||  ||||||| ||||||
Db       3180 AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3239

Qy       3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
              ||||| || ||||| |||||||||||||||||||||||| ||||| ||||||||||||
Db       3240 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3299

Qy       3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
              ||||| ||||| |||||||| ||||||||||||||||||||||||||||||||||||||
Db       3300 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3359

Qy       3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
              ||| | |||||||||||||||||||| ||||| |||||||||| ||||||||||||||
Db       3360 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3419

Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
              |||||||||||||||| |||| ||||| ||||| ||||| || ||||||||||||||||||
Db       3420 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3479

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
              |||||||| |||||||||||||||||||||||||| ||||| ||||||||||||||||
Db       3480 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3539

Qy       3571 AATGGTCTGACAC          TAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
              |||||||||||||||||||||| ||||| || |||||||||||| ||||||||||||||
Db       3540 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3599

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
              |||||||||||||  |||||||||||||||||||||||||||||| |||| |||||| |||
Db       3600 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3659

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
              || ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db       3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709
```

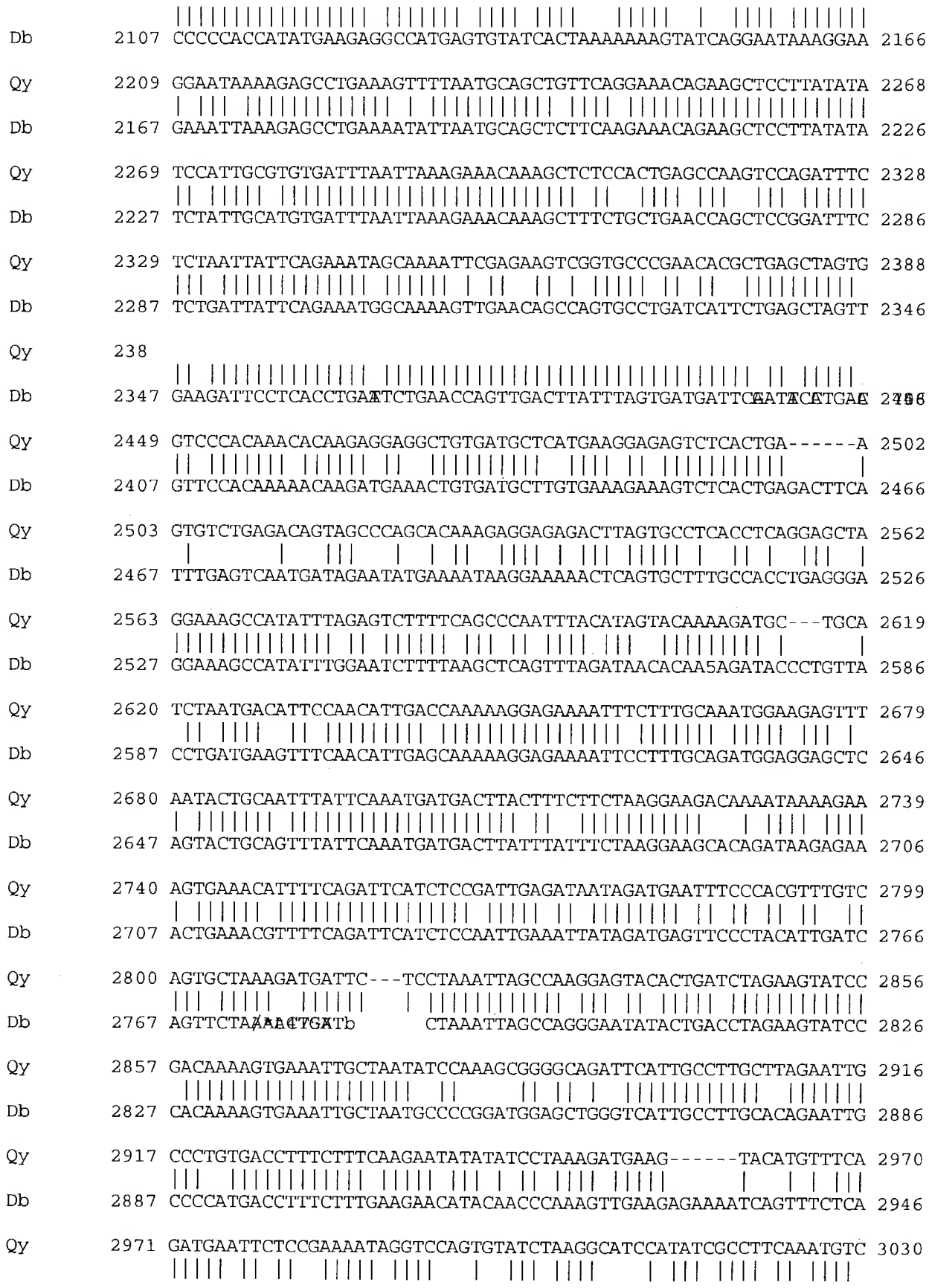
RESULT 4
US-10-060-036-53
; Sequence 53, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53

Query Match 62.6%; Score 2343.6; DB 15; Length 4632;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

```
Qy        134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
              | || ||| | | |||  ||||||  ||||| | ||||||||||||||||||||||| ||
Db         23 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 82

Qy        194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
              |||||  |  ||  |  | |||||||| | |||||||||||| ||  | |||| ||||||
Db         83 CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 141

Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
              ||||||||| | ||||||||  | |||||   ||||||| |||||||||| ||||||||
Db        142 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 198

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | ||||||  |||||||||||||||||||  |||||||||||||||||||   || || |||
Db        199 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 255

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              ||||||||  ||||||||  ||  |||||  |||||  |||||  ||||||||||||||||||||
Db        256 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 315

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486
              |||||  ||||||||||||||  ||  | ||||      | ||  |||||||  ||||||  |||
Db        316 CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 375

Qy        487 CTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
              ||||||||  | |  ||||  |||||  ||  ||||||||  ||  ||  ||||||||||  |||
Db        376 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 435
```


Qy 547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG---------CGGCGCCC 597
Db 436 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 495
Qy 598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
Db 496 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 555
Qy 658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG------ 711
Db 556 CCTCCGGCCCGGCCTCCCCCTCCTCCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 615
Qy 712 ----------CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
Db promo616 225XC CAGCCCCGGCTCCCGCCGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGC 675
Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
Db 676 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 735
Qy 808 GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
Db 736 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 792
Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927
Db 793 TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT 852
Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987
Db 853 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 912
Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
Db 913 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 972
Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107
Db 973 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1032
Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167
Db 1033 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1092
Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
Db 1093 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1152
Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT---------------GTGGGTAAAGAAGAC 1269
Db 1153 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1212
Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTA 1329
Db 1213 GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAA 1272

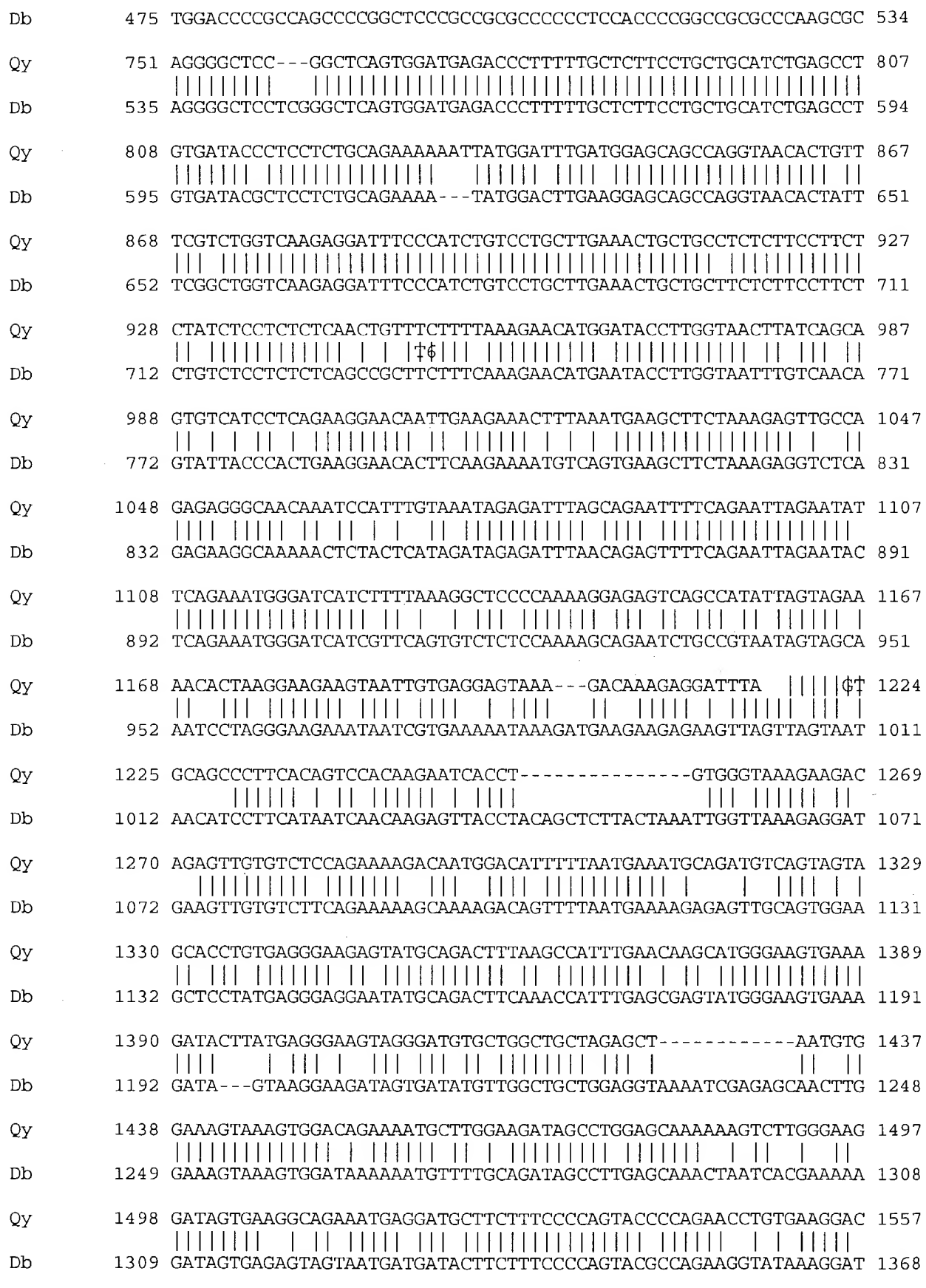


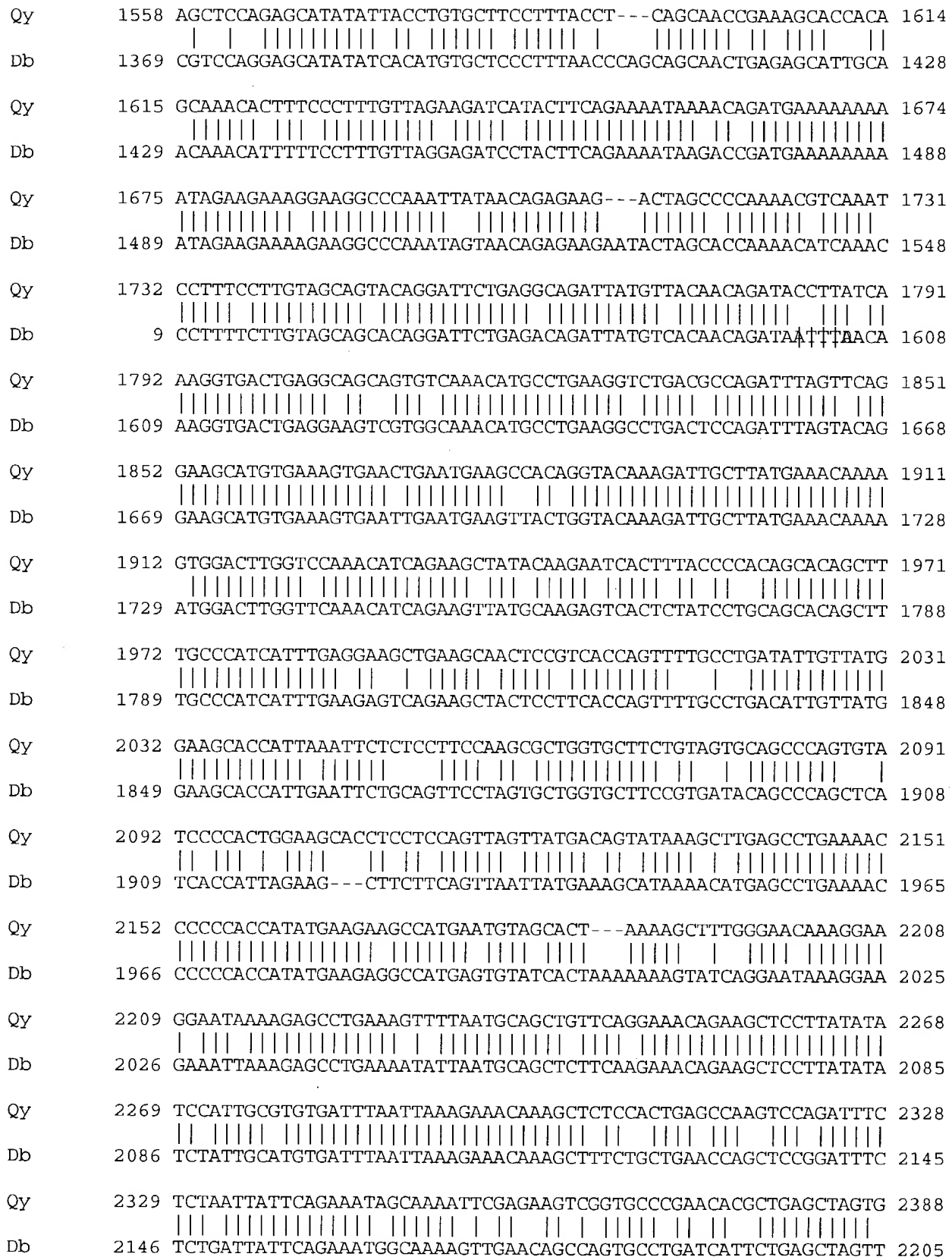


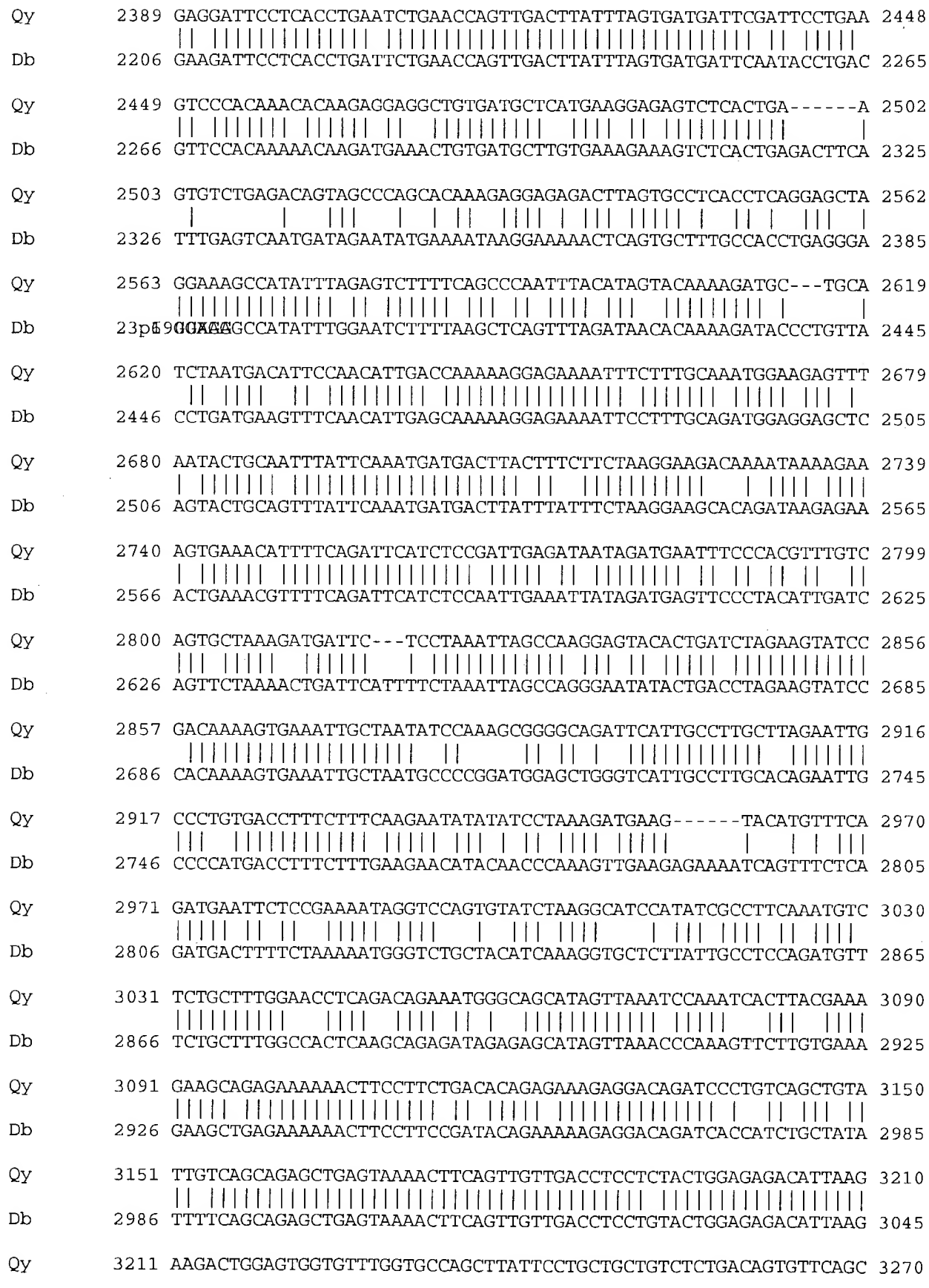
```
Db       2947 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 3006

Qy       3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
             ||||||||||   ||||  ||||  ||  |  ||||||||||||  |||||   |||  ||||
Db       3007 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 3066

Qy       3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150
             |||||  ||||||||||||||||||  ||  |||||  ||||||||||||||  |  ||  ||| ||
Db       3067 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 3126

Qy       3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
             ||  ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db       3127 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3186

Qy       3211 AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3270
             |||||||||||||||||||||||||||  ||||||||||||  ||  |||||||  ||||||
Db       3187 AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3246

Qy       3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
             |||||  ||  |||||  |||||||||||||||||||||||||  |||||  ||||||||||||
Db       3247 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3306

Qy       3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
             |||||  |||||  ||||||||  ||||||||||||||||||||||||||||||||||||||
Db       3307 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3366

Qy       3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
             |||  |  ||||||||||||||||||||  |||||  ||||||||||  ||||||||||||||||
Db       3367 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3426

Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTC050XA   GTATTGA 3510
             ||||||||||||||||  ||||  |||||  |||||  |||||  ||  ||||||||||||||||||
Db       3427 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3486

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
             ||||||||  ||||||||||||||||||||||||||  |||||  ||||||||||||||||||
Db       3487 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3546

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
             ||||||||||||||||||||||  |||||  ||  ||||||||||||  ||||||||||||||
Db       3547 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3606

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
             ||||||||||||  ||||||||||||||||||||||||||||||  ||||  ||||||  |||
Db       3607 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3666

Qy       3691 GCCATGGCCAAAATC        AAATCCCTGGATTGAAGCGCAAAGCAGA 37AAC     477
             ||  ||||||  ||||||||||||||||||||||||||||||||||||||||  ||
Db       3667 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3716
```

RESULT 5
US-09-789-386-1
; Sequence 1, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID

```
;  APPLICANT:  PRINJHA, RABINDER KUMAR
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP-30165-C1
;  CURRENT APPLICATION NUMBER: US/09/789,386
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: U.K. 9916898.1
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: U.K. 9816024.5
;  PRIOR FILING DATE: 1998-07-22
;  PRIOR APPLICATION NUMBER: US 09/359,208
;  PRIOR FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 3579
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-789-386-1

  Query Match             61.2%;  Score 2289.2;  DB 9;  Length 3579;
  Best Local Similarity   81.5%;  Pred. No. 0;
  Matches 2925;  Conservative    0;  Mismatches  548;  Indels  117;  Gaps   19;

Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCC¢GCCCCGGC¢†|
              |||||||||  | ||||||||  | |||||  ||||||| |||||||||| ||||||||
Db          1 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 57

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| |||||||||||||||||| |||||||||||||||||   || || |||
Db         58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486
              ||||| |||||||||||||| ||  | ||||      | || ||||||| |||||| |||
Db        175 CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 234

Qy        487 CTGGACTTCAGCAGCGACTCGGTGCCCCCCGCG
               |||||||| | |  ||||  ||||| || |||||||| || || |||||||||| |||
Db        235 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy        547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG---------CGGCGCCC 597
              || | ||| || ||| ||||||| || ||||| |  ||||| |         | | ||||
Db        295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 354

Qy        598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
              |||||||||| || | | |||||||||||  |||||||||||||| ||||||||||||
Db        355 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy        658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG------ 711
              ||||||||  |||| || ||||| || || ||| ||| |||||||| ||| |||
Db        415 CCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474

Qy        712 ----------------------CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
                                   |||||||||||||$0¥|||| ||¢¢†¢¢¢¢¢¢¢¢¢¢¢¢ 546
```



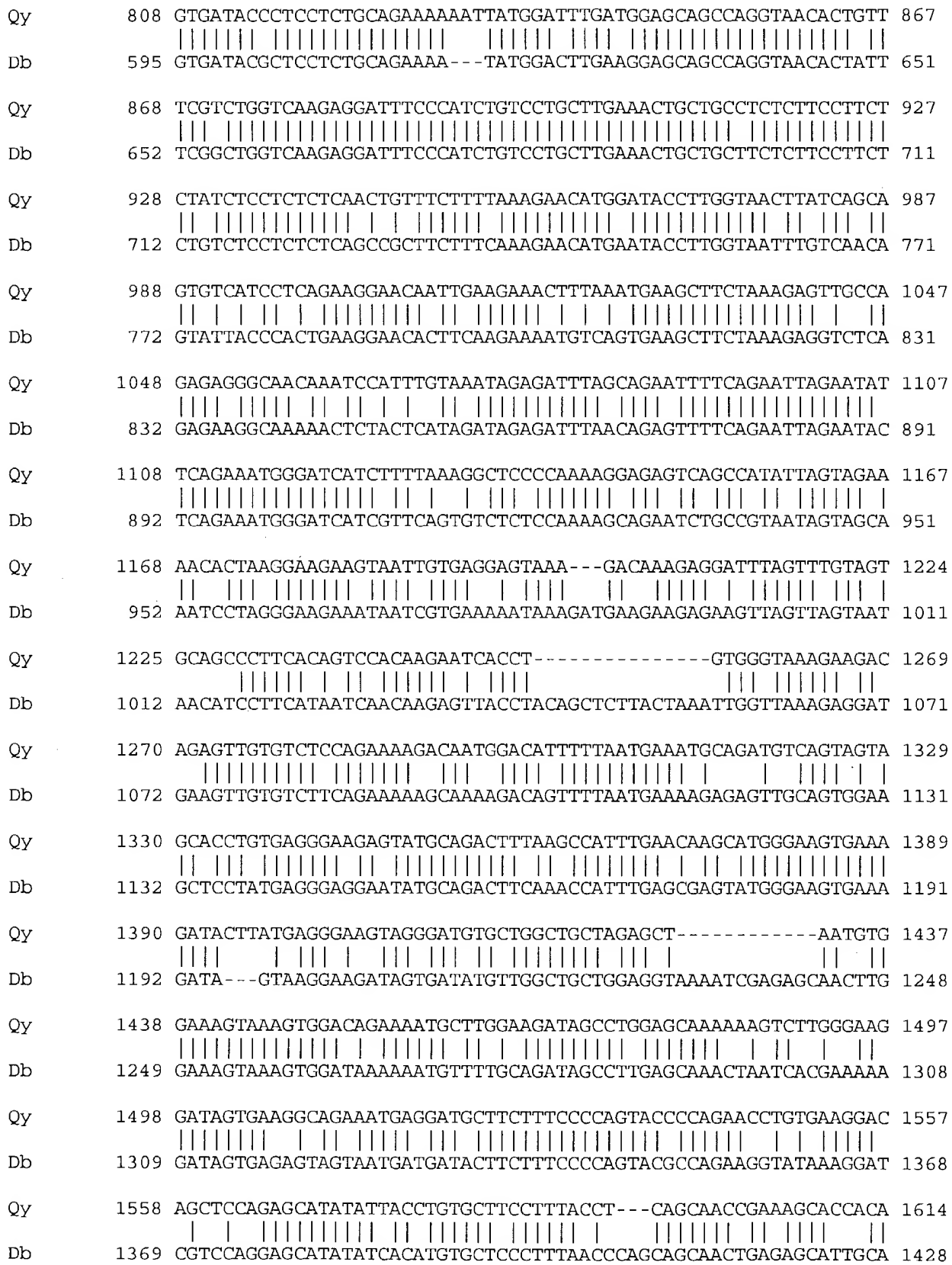


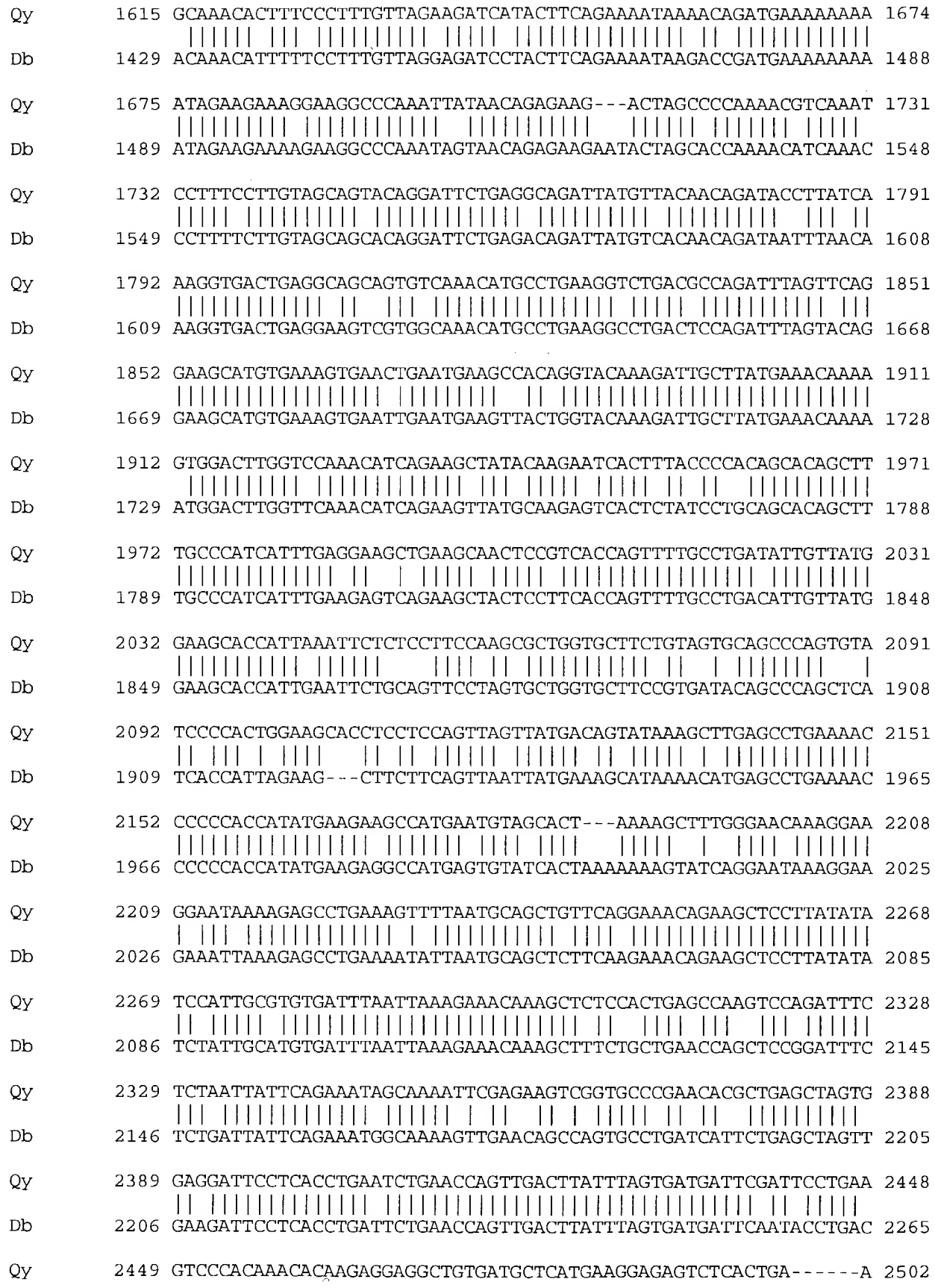


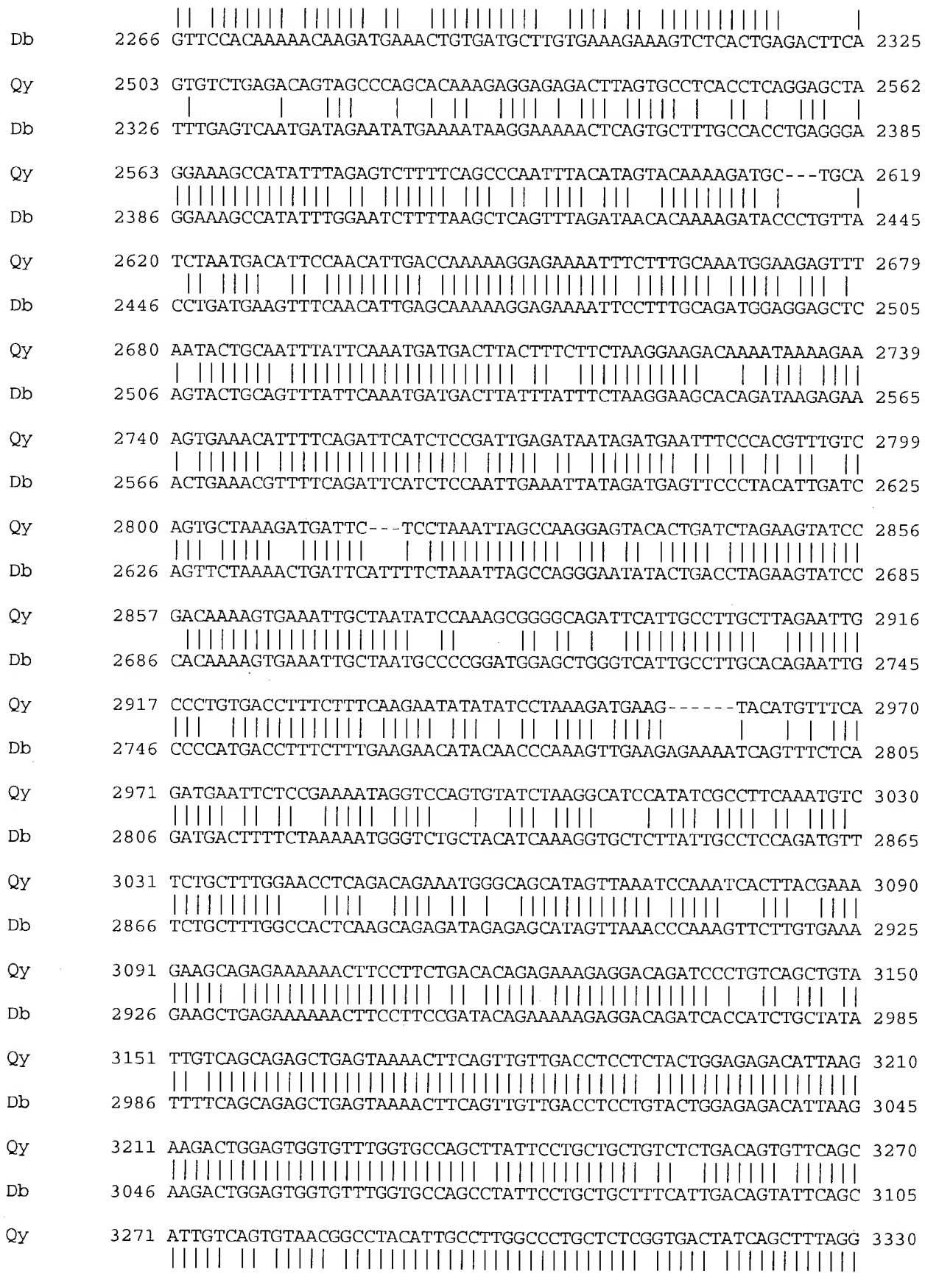
```
                ||||||||||||||||||||||||||| |||||||||||| ||  ||||||| ||||||
Db       3046 AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3105

Qy       3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
                ||||| || ||||| ||||||||||||||||||||||||| ||||| ||||||||||||
Db       3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165

Qy       3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
                ||||| ||||| |||||||| ||||||||||||||||||||||||||||||||||||||
Db       3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3225

Qy       3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
                ||| | |||||||||||||||||| ||||| |||||||||| ||||||||||||||||
Db       3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285

Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
                ||||||||||||||| |||| ||||| ||||| ||||| || ||||||||||||||||||
Db       3286 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
                |||||||| |||||||||||||||||||||||| ||||| ||||||||||||||||||
Db       3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
                |||||||||||||||||||||| ||||| || |||||||||||| ||||||||||||||
Db       3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
                |||||||||||||| |||||||||||||||||||||||||||||| |||| |||||| |||
Db       3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
                || ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db       3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575
```

RESULT 6
US-09-893-348-22
; Sequence 22, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21

```
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 3579
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3579)
;   OTHER INFORMATION:
US-09-893-348-22

  Query Match             61.2%;  Score 2289.2;  DB 9;  Length 3579;
  Best Local Similarity   81.5%;  Pred. No. 0;
  Matches 2925;  Conservative    0;  Mismatches  548;  Indels  117;  Gaps   19;

Qy        253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
              ||||||||| | ||||||||  | |||||  ||||||| |||||||||| ||||||||
Db          1 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 57

Qy        313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
              | |||||| ||||||||||||||||||| ||||||||||||||||||    || || |||
Db         58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy        373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
              |||||||| |||||||| || ||||| ||||| ||||| ||||||||||||||||||||
Db        115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy        433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC------CGCCCGCCGCCGCCGCGCCGCTG 486
              ||||| |||||||||||||| ||  | ||||      | || ||||||| |||||| |||
Db        175 CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTG 234

Qy        487 CTGGACTTCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
              |||||||| | |  |||| ||||| || |||||||| || || |||||||||| |||
Db        235 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy        547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG---------CGGCGCCC 597
              || | ||| || ||| ||||||| || ||||| |  ||||| |          | | ||||
Db        295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 354

Qy        598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
              |||||||||| || | | |||||||||||  |||||||||||||| ||||||||||||
Db        355 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy        658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG------ 711
              ||||||||  |||| || ||||| || || ||| ||| |||||||| ||| |||
Db        415 CCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474

Qy        712 ----------------------CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
                                   |||||||||||||| ||||| ||||||||||||||||||
Db        475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGC 534

Qy        751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 594
```







```
Db       3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165

Qy       3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
              ||||| ||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db       3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3225

Qy       3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
              ||| | |||||||||||||||||||| ||||| |||||||||| ||||||||||||||||
Db       3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285

Qy       3451 CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
              |||||||||||||||| |||| ||||| ||||| ||||| || ||||||||||||||||||
Db       3286 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345

Qy       3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC 3570
              |||||||| |||||||||||||||||||||||| ||||| ||||||||||||||||||
Db       3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405

Qy       3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
              |||||||||||||||||||||||| ||||| || |||||||||||| ||||||||||||||
Db       3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465

Qy       3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
              |||||||||||| |||||||||||||||||||||||||||||| |||| |||||| |||
Db       3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525

Qy       3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
              || |||||| |||||||||||||||||||||||||||||||||||||||| ||
Db       3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575
```

RESULT 7
US-10-220-891-22
; Sequence 22, Application US/10220891
; Publication No. US20030207286A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERITICS OF ENHANCED
; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE
PROGNOSIS
; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH
FAVORABLE
; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE
PROGNOSIS
; FILE REFERENCE: 7388-73435
; CURRENT APPLICATION NUMBER: US/10/220,891
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000/140387
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/159195
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-220-891-22

Query Match 29.1%; Score 1088.8; DB 13; Length 1980;
Best Local Similarity 83.5%; Pred. No. 1.3e-269;
Matches 1289; Conservative 0; Mismatches 237; Indels 18; Gaps 4;

```
Qy       2215 AAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATATCCATT 2274
             ||||||||||||| | |||||||||||| |||| |||||||||||||||||||||||| |||
Db         28 AAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT 87

Qy       2275 GCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAAT 2334
             || |||||||||||||||||||||||||| ||  |||| |||  ||| ||||||||| ||
Db         88 GCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGAT 147

Qy       2335 TATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGAT 2394
             |||||||||| |||||| | ||  || | ||||| || ||  |||||||||| || |||
Db        148 TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGAT 207

Qy       2395 TCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCA 2454
             |||||||||| |||||||||||||||||||||||||||||||| || ||||| || |||
Db        208 TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA 267

Qy       2455 CAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA------AGTGTCT 2508
             |||| |||||  ||  |||||||||  |||| || ||||||||||      | |
Db        268 CAAAAACAAGGTGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAG 327

Qy       2509 GAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAG 2568
                |  |||   |  | ||  |||| | ||| ||||| |  || |  |||  |||||||
Db        328 TCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAG 387

Qy       2569 CCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCATCTAAT 2625
             |||||||| || |||||| ||| || |||| |||  ||||||||| |      | || ||
Db        388 CCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGAT 447

Qy       2626 GACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACT 2685
             ||  || ||||||||| |||||||||||||||| ||||||| ||||| ||| | | ||||
Db        448 GAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACT 507

Qy       2686 GCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAA 2745
             ||| |||||||||||||||||| ||  |||||||||||   | |||| ||||| ||||
Db        508 GCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAA 567

Qy       2746 ACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCT 2805
             || |||||||||||||||| ||||| || |||||||| || || || ||  ||||| ||
Db        568 ACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTCCT 627

Qy       2806 AAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAA 2862
             |||  ||||||   | |||||||||||| ||| || ||||| |||||||||||| |||||
Db        628 AAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAA 687

Qy       2863 AGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGT 2922
             ||||||||||||||  ||      || || |  |||||||||||  |||||||||  |
Db        688 AGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCAT 747

Qy       2923 GACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG------TACATGTTTCAGATGAA 2976
             |||||||||| ||||| ||| | || |||| |||||      |   | | ||||||||
Db        748 GACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGAC 807
```

```
Qy       2977 TTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCT 3036
              ||  ||  ||||| ||||    |  ||| ||||    | ||| |||| || |||| ||||||
Db        808 TTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCT 867

Qy       3037 TTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCA 3096
              ||||   ||||| |||| || |  |||||||||||| |||||   |||  |||||||||
Db        868 TTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCT 927

Qy       3097 GAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCA 3156
              ||||||||||||||||| || ||||| |||||||||||||| |  || ||| |||| |||
Db        928 GAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCA 987

Qy       3157 GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACT 3216
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        988 GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACT 1047

Qy       3217 GGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTC 3276
              |||||||||||||||||||| |||||| |||||| ||  ||||||| ||||||||||
Db       1048 GGAGTGGTGTTTGGTGCCAGCCTATTCCAGCTGCTTTCATTGACAGTATTCAGCATTGTG 1107

Qy       3277 AGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATAT 3336
              ||  ||||| |||||||||||||||||||||||||| ||||| ||||||||||||||||
Db       1108 AGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAC 1167

Qy       3337 AAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTA 3396
              |||||  |||||||| |||||||||||||||||||||||||||||||||||||||||| |
Db       1168 AAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTG 1227

Qy       3397 GAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGT 3456
              |||||||||||||||||| ||||| |||||||||| ||||||||||||||||||||
Db       1228 GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGT 1287

Qy       3457 CATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGAT 3516
              |||||||||  |||| ||||| ||||| ||||| || ||||||||||||||||||||||
Db       1288 CATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT 1347

Qy       3517 TCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGT 3576
              ||  ||| |||||||||||||||||||| ||||| |||||||||||||||| ||||||
Db       1348 TCTCTGGAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGT 1407

Qy       3577 CTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGG 3636
              |||||||||||||||| ||||| || |||||||||||| ||||||||||||||||||||
Db       1408 CTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGG 1467

Qy       3637 CATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATG 3696
              |||||||  |||||||||||||||||||||||||||| |||| |||||| ||||| |||
Db       1468 CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG 1527

Qy       3697 GCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
              || ||||||||||||||||||||||||||||||||||||||| ||
Db       1528 GCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 1571
```

RESULT 8
US-10-205-194-165
; Sequence 165, Application US/10205194

; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 165
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-165

Query Match 21.6%; Score 809.8; DB 13; Length 2782;
Best Local Similarity 99.8%; Pred. No. 1.7e-197;
Matches 811; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          14 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 73
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         462 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 521

Qy          74 CAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG 133
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         522 GAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG 581

Qy         134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         582 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 641

Qy         194 CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA 253
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         642 CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA 701

Qy         254 TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC 313
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         702 TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC 761

Qy         314 CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG 373
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         762 CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG 821

Qy         374 AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC 433
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         822 AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC 881

Qy         434 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCGCCGCTGCTGGACT 493
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        882 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCGCCGCTGCTGGACT 941

Qy        494 TCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 TCAGCAGCGACTCGGTGCCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 1001

Qy        554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 1061

Qy        614 CCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1062 CCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 1121

Qy        674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1122 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 1181

Qy        734 CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTG 793
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1182 CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTG 1241

Qy        794 CTGCATCTGAGCCTGTGATACCCTCCTCTGCAG 826
              |||||||||| ||||||||||||||||||||||
Db       1242 CTGCATCTGAACCTGTGATACCCTCCTCTGCAG 1274
```

```
RESULT 9
US-09-789-386-5
; Sequence 5, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
;  APPLICANT: MICHALOVICH, DAVID
;  APPLICANT:  PRINJHA, RABINDER KUMAR
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP-30165-C1
;  CURRENT APPLICATION NUMBER: US/09/789,386
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: U.K. 9916898.1
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: U.K. 9816024.5
;  PRIOR FILING DATE: 1998-07-22
;  PRIOR APPLICATION NUMBER: US 09/359,208
;  PRIOR FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 1122
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-789-386-5

  Query Match             13.3%;  Score 497.4;  DB 9;  Length 1122;
  Best Local Similarity   92.7%;  Pred. No. 3.4e-117;
  Matches  522;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       3178 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 3237
```

```
                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          556 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 615

Qy         3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297
                ||||||||||||| ||  ||||||| |||||||||| || ||||| ||||||||||||
Db          616 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 675

Qy         3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
                |||||||||||||| ||||| |||||||||||||||||| ||||| |||||||| ||||||
Db          676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735

Qy         3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
                |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db          736 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 795

Qy         3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
                ||||| |||||||||||| |||||||||||||||||||||||||||||| |||| |||||
Db          796 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 855

Qy         3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
                ||||| ||||| || |||||||||||||||||||||||| ||||||||||||||||||
Db          856 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 915

Qy         3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
                |||||||| ||||| |||||||||||||||| |||||||||||||||||||||| |||
Db          916 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 975

Qy         3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
                || || |||||||||||| |||||||||||||||||||||||||  ||||||||||||
Db          976 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035

Qy         3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
                |||||||||||||||| |||| |||||| ||||| ||||| ||||||||||||||||||
Db         1036 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1095

Qy         3718 CCTGGATTGAAGCGCAAAGCAGA 3740
                ||||||||||||||||||| ||
Db         1096 CCTGGATTGAAGCGCAAAGCTGA 1118
```

RESULT 10
US-10-175-523-156
; Sequence 156, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/1J795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151

; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
;   LENGTH: 1160
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-175-523-156

Query Match 13.3%; Score 497.4; DB 15; Length 1160;
Best Local Similarity 92.7%; Pred. No. 3.5e-117;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
Qy       3178 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 3237
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 287

Qy       3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297
             |||||||||||||  ||  ||||||| |||||||||||  ||  |||||  ||||||||||||
Db        288 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 347

Qy       3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
             |||||||||||||| |||||  |||||||||||||||||  |||||  ||||||||  ||||||
Db        348 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 407

Qy       3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
             |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        408 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 467

Qy       3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
             |||||  ||||||||||| |||||||||||||||||||||||||||||  ||||  |||||
Db        468 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 527

Qy       3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
             |||||  |||||  ||  |||||||||||||||||||||||  ||||||||||||||||||
Db        528 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 587

Qy       3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
             ||||||||  |||||  ||||||||||||||||  |||||||||||||||||||||||  |||
Db        588 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 647

Qy       3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
             ||  ||  ||||||||||| |||||||||||||||||||||||||  ||||||||||||
Db        648 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 707

Qy       3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
             ||||||||||||||||  ||||  ||||||  |||||  |||||  ||||||||||||||||||
```

```
Db        708 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 767

Qy       3718 CCTGGATTGAAGCGCAAAGCAGA 3740
              ||||||||||||||||||||| ||
Db        768 CCTGGATTGAAGCGCAAAGCTGA 790


RESULT 11
US-10-439-388-62
; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
;  APPLICANT: Aune, Thomas M
;  APPLICANT:  Olsen, Nancy J
;  TITLE OF INVENTION: Method for Predicting Autoimmune Disease
;  FILE REFERENCE: 1242/68
;  CURRENT APPLICATION NUMBER: US/10/439,388
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: US 60/381,055
;  PRIOR FILING DATE: 2002-05-16
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 1785
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-439-388-62

  Query Match             13.3%;  Score 497.4;  DB 12;  Length 1785;
  Best Local Similarity   92.7%;  Pred. No. 4.8e-117;
  Matches  522;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       3178 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 3237
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 306

Qy       3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297
              |||||||||||| ||  ||||||| |||||||||| || ||||| ||||||||||||
Db        307 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 366

Qy       3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
              |||||||||||||| ||||| |||||||||||||||| ||||| |||||||| ||||||
Db        367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 426

Qy       3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
              |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        427 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 486

Qy       3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
              ||||| |||||||||| ||||||||||||||||||||||||||||| |||| |||||
Db        487 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 546

Qy       3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
              ||||| ||||| || |||||||||||||||||||||||| ||||||||||||||||||
Db        547 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 606

Qy       3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
```

```
                ||||||||  |||||  ||||||||||||||||  ||||||||||||||||||||||  |||
Db          607 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 666

Qy         3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
                || ||  ||||||||||||  ||||||||||||||||||||||||||||  ||||||||||||
Db          667 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 726

Qy         3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
                ||||||||||||||||  ||||  ||||||  |||||  |||||  ||||||||||||||||||
Db          727 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 786

Qy         3718 CCTGGATTGAAGCGCAAAGCAGA 3740
                ||||||||||||||||||||  ||
Db          787 CCTGGATTGAAGCGCAAAGCTGA 809
```

RESULT 12
US-10-060-036-54
; Sequence 54, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-54

Query Match 13.3%; Score 497.4; DB 15; Length 2235;
Best Local Similarity 92.7%; Pred. No. 5.7e-117;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
Qy         3178 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 3237
                ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db          697 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 756

Qy         3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297
                ||||||||||||||  ||  |||||||  ||||||||||||  ||  |||||  ||||||||||||
Db          757 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 816

Qy         3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
                ||||||||||||||  |||||  ||||||||||||||||  |||||  ||||||||  ||||||
Db          817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 876

Qy         3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
```

```
                ||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        877 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 936

Qy       3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
                ||||| |||||||||||| |||||||||||||||||||||||||||||| |||| |||||
Db        937 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 996

Qy       3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
                ||||| ||||| || |||||||||||||||||||||||||| ||||||||||||||||||
Db        997 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 1056

Qy       3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
                |||||||| ||||| |||||||||||||||| |||||||||||||||||||||||| |||
Db       1057 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 1116

Qy       3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
                || || |||||||||||| |||||||||||||||||||||||||||  ||||||||||||
Db       1117 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1176

Qy       3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
                |||||||||||||||| |||| |||||| ||||| ||||| ||||||||||||||||||
Db       1177 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1236

Qy       3718 CCTGGATTGAAGCGCAAAGCAGA 3740
                |||||||||||||||||||| ||
Db       1237 CCTGGATTGAAGCGCAAAGCTGA 1259
```

```
RESULT 13
US-09-765-205-5
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Li
;  TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
;  FILE REFERENCE: 1458.004/200130.449
;  CURRENT APPLICATION NUMBER: US/09/765,205
;  CURRENT FILING DATE:  2001-01-17
;  PRIOR APPLICATION NUMBER: US/09/212,440
;  PRIOR FILING DATE: 1998-12-16
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 1610
;   TYPE: DNA
;   ORGANISM: human
US-09-765-205-5

  Query Match             13.3%;  Score 495.8;  DB 9;  Length 1610;
  Best Local Similarity   92.5%;  Pred. No. 1.2e-116;
  Matches  521;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy       3178 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 3237
                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        687 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGC 746

Qy       3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297
```

```
                |||||||||||||| ||  ||||||| |||||||||||| || ||||| ||||||||||||
Db        747 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 806

Qy       3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
                |||||||||||||| ||||| |||||||||||||||| ||||| |||||||| ||||||
Db        807 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 866

Qy       3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
                |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        867 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 926

Qy       3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
                ||||| |||||||||| |||||||||||||||||||||||||| ||| |||| |||||
Db        927 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTCAACTGCACGATAAAG 986

Qy       3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
                ||||| ||||| || |||||||||||||||||||||||| ||||||||||||||||||
Db        987 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 1046

Qy       3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
                |||||||| ||||| |||||||||||||||| |||||||||||||||||||||||| |||
Db       1047 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 1106

Qy       3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
                || || |||||||||||| |||||||||||||||||||||||||  ||||||||||||
Db       1107 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1166

Qy       3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
                |||||||||||||||| |||| |||||| ||||| ||||| ||||||||||||||||||
Db       1167 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1226

Qy       3718 CCTGGATTGAAGCGCAAAGCAGA 3740
                |||||||||||||||||||| ||
Db       1227 CCTGGATTGAAGCGCAAAGCTGA 1249
```

RESULT 14
US-09-789-386-3
; Sequence 3, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 868

; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (91)(413)
US-09-789-386-3

Query Match 12.9%; Score 483.6; DB 9; Length 868;
Best Local Similarity 76.8%; Pred. No. 1e-113;
Matches 668; Conservative 0; Mismatches 166; Indels 36; Gaps 5;

```
Qy        830 AAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCC 889
              ||| |||||| |||| |||||||||||||||||| ||||| ||||||||||||||||||
Db          2 AAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTCGGCTGGTCAAGAGGATTTCC 61

Qy        890 CATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTT 949
              ||||||||||||||||||||||||| ||| |||||||||| |||||||||||| | | ||
Db         62 CATCTGTCCTGCTTGAAACTGCTGCTTCTNTTCCTTCTCTGTCTCCTCTCTCAGCCGCTT 121

Qy        950 CTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCATCCTCAGAAGGAACAA 1009
              |||| |||||||||| |||||||||||  || ||| |||| | | || | |||||||||
Db        122 CTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCCACTGAAGGAACAC 181

Qy       1010 TTGAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTG 1069
              || |||||| | | | ||||||||||||||||| |  |||||| ||||| || || | |
Db        182 TTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAAGGCAAAAACTCTACTCA 241

Qy       1070 TAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTA 1129
              || |||||||||||| |||| |||||||||||||||| |||||||||||||||| || |
Db        242 TAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATGGGATCATCGTTCA 301

Qy       1130 AAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTG 1189
                | ||| ||||||| ||| || ||| || |||||| |||  ||| ||||||| |||| |
Db        302 GTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCAAATCCTAGGGAAGAAATAATCG 361

Qy       1190 TGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAG 1246
              |||  | ||||   ||  ||||| | |||||| ||| |     |||||| | || |||||
Db        362 TGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAATAACATCCTTCATANTCAACAAG 421

Qy       1247 AATCACCT---------------GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGA 1291
              | | ||||                 ||| |||||| ||   |||||||||| |||||||
Db        422 AGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTGTGTCTTCAGAAAAAG 481

Qy       1292 CAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATG 1351
              |||  |||| |||||||||| |    |  |||| | ||| ||| ||||||| || ||||
Db        482 CAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATGAGGGAGGAATATG 541

Qy       1352 CAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGG 1411
              ||||||| || |||||||| | || |||||||||||||||||    | ||| |  ||| |
Db        542 CAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAGATA---GTAAGGAAGATAGTG 598

Qy       1412 ATGTGCTGGCTGCTAGAGCT------------AATGTGGAAAGTAAAGTGGACAGAAAAT 1459
              || || |||||||| ||| |            ||  |||||||||||||||| | |||||
Db        599 ATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTGGAAAGTAAAGTGGATAAAAAAT 658

Qy       1460 GCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGATAGTGAAGGCAGAAATGAGG 1519
              | || | ||||||||| |||||||  | ||  |  || ||||||||  | || |||||
```

```
Db        659 GTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAGTGAGAGTAGTAATGATG 718

Qy       1520 ATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGCTCCAGAGCATATATTACCT 1579
              || ||||||||||||||||| ||||||  | | |||||  | ||  |||||||||| || |
Db        719 ATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTTCAGGAGCATATATCACAT 778

Qy       1580 GTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACAGCAAACACTTTCCCTTTGTTAG 1636
              ||||| ||||||   |  ||||||| || ||||   || |||||| ||| ||||||||||
Db        779 GTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCAACAAACATTTTTCCTTTGTTAG 838

Qy       1637 AAGATCATACTTCAGAAAATAAAACAGATG 1666
              ||||| |||||||||||||| || ||||
Db        839 GAGATCCTACTTCAGAAAATAAGACCGATG 868


RESULT 15
US-09-960-352-8477
; Sequence 8477, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH
LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8477
;   LENGTH: 422
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 36-LIB34-048-Q1-E1-A8
US-09-960-352-8477

  Query Match             10.0%;  Score 375.6;  DB 10;  Length 422;
  Best Local Similarity   93.1%;  Pred. No. 4.3e-86;
  Matches  393;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       3282 AACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGG 3341
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 AACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGG 60

Qy       3342 CGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATC 3401
              |||||||||||||||||||||| |||||||||||||||||||||||||||| |||||
Db         61 TGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATC 120

Qy       3402 TGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGT 3461
              |||||||||||||| ||||| |||||||||| ||||| ||||||||||||||||||||
Db        121 TGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGT 180

Qy       3462 GAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCT 3521
              ||| |||||||||||||| || || || |||||||||||||||||||||||||| ||
Db        181 TAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCT 240
```

```
Qy       3522 GAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGAC 3581
              ||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||
Db        241 GAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGAC 300

Qy       3582 ACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCA 3641
              |||||| ||||| |||||||| |||||||||||| ||||||||||||||||||||||||
Db        301 ACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCA 360

Qy       3642 GGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAA 3701
              || ||| |||||||||||||| |||||||||| |||| |||||| ||||| ||||| ||
Db        361 GGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAA 420

Qy       3702 AA 3703
              ||
Db        421 AA 422
```

Search completed: January 23, 2004, 15:24:40
Job time : 1133.66 secs